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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 31 Seconds

(without alignments)
902.922 Million cell updates/sec

Title: US-09-910-033a-2

Perfect score: 1290

Sequence: 1 MSRLDGKVAITGTGLG.....NESKATGSEFVVDGGYTAQ 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	99.0	252	18 AAW23407	Lactobacillus brev
2	1019	79.0	251	18 AAW23409	Lactobacillus kefi
3	456	35.3	254	22 AAB49773	Protein with acety
4	450	34.9	254	22 AAB47522	(R)-2-octanol dehy
5	400	31.0	258	21 AAY56815	Bacillus D-arabini
6	369	28.6	272	22 AAU37095	Staphylococcus aur
7	367.5	28.5	261	13 AAR27757	Glucose dehydrogen
8	364.5	28.3	261	11 AAR04044	Glucose dehydrogen
9	364.5	28.3	261	13 AAR24018	Thermostable gluc
10	364	28.2	251	22 AAU34193	Staphylococcus aur
11	363.5	28.2	272	21 AAB10740	B. megaterium gluc

12	363.5	28.2	340	21 AAB10741	H. ghiliani/B. me
13	360.5	27.9	261	11 AAR03846	Modified glucose d
14	359.5	27.9	261	13 AAR27756	NAD affinity gluc
15	358.5	27.8	261	9 AAP80590	Sequence of glucos
16	358.5	27.8	261	21 AAY96271	B. subtilis glucos
17	358.5	27.8	261	21 AAY54424	Amino acid sequenc
18	356.5	27.6	261	9 AAP80063	Glucose dehydrogen
19	352.5	27.3	262	22 AAG83032	S. epidermidis ope
20	351	27.2	286	22 AAG36267	Pseudomonas aerugi
21	345	26.7	306	22 AAG81844	S. epidermidis ope
22	344	26.7	270	21 AAB42558	Human ORFX ORF2322
23	340	26.4	270	20 AAY41761	Human PROA74 prote
24	340	26.4	270	21 AAB44317	Human PROA74 (UNQ5
25	340	26.4	270	21 AAB24056	Human PROA74 prote
26	340	26.4	270	22 AAU28108	Novel human secret
27	340	26.4	279	22 AAU18296	Human endocrine po
28	336.5	26.1	271	22 AAU37794	Streptococcus pneu
29	336.5	26.1	272	22 AAU38086	Streptococcus pneu
30	334.5	25.9	288	22 AAU28296	Novel human secret
31	330.5	25.6	277	21 AAY54415	Secoisolaricresin
32	324	25.1	336	16 AAW06488	Maize Tsz sequence
33	322	25.0	286	21 AAY25099	Human OXRE-6. Hom
34	319.5	24.8	256	17 AAW02111	Glucuronate:NADP+-5-
35	317.5	24.6	262	20 AAY08329	A. parasiticus ver
36	317.5	24.6	263	22 AAG81555	S. epidermidis ope
37	317	24.6	241	12 AAR10679	Acetoacetyl CoA re
38	317	24.6	300	21 AAG18620	Arabidopsis thalia
39	317	24.6	343	21 AAG18619	Arabidopsis thalia
40	316	24.5	248	21 AAY54422	Amino acid sequenc
41	314	24.3	283	21 AAG31552	Arabidopsis thalia
42	312.5	24.2	260	17 AAR94617	3-hydroxybutyric a
43	311.5	24.1	253	22 AAU36249	Pseudomonas aerugi
44	311.5	24.1	289	22 AAG83109	S. epidermidis ope
45	309.5	24.0	272	21 AAG09589	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAW23407	AAW23407 standard; Protein; 252 AA.
ID	AAW23407
XX	AAW23407;
AC	AAW23407;
XX	27-MAR-1998 (first entry).
DT	Lactobacillus brevis alcohol dehydrogenase.
XX	Lactobacillus brevis
DE	Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.
XX	Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.
KW	Lactobacillus brevis
XX	Lactobacillus brevis
OS	Lactobacillus brevis
XX	EP796914-A2.
PN	24-SEP-1997.
XX	24-SEP-1997.
PD	20-MAR-1997; 97EP-0104814.
XX	20-MAR-1997; 97EP-0104814.
PF	21-MAR-1996; 96DE-4010984.
XX	21-MAR-1996; 96DE-4010984.
PR	(BOEF) BOEHRINGER MANNHEIM GMBH.
XX	(BOEF) BOEHRINGER MANNHEIM GMBH.
PA	Hummel W, Riebel B;
XX	Hummel W, Riebel B;
PI	WPI; 1997-459831/43.
XX	(R)-2-octanol dehy
DR	N-PSDB; AAT73132.
XX	N-PSDB; AAT73132.
XX	Staphylococcus aur
PT	Glucose dehydrogen
XX	Glucose dehydrogen
PT	Thermostable gluc
XX	Thermostable gluc
PS	Staphylococcus aur
XX	Staphylococcus aur
PS	B. megaterium gluc
XX	B. megaterium gluc

Claim 8; Pages 24-26; 34pp; German.

CC The present sequence is a Lactobacillus brevis alcohol
 CC dehydrogenase, which retains at least 95% of its activity after 30
 CC minutes at 20-60 degrees C and can be purified to a specific
 CC activity of at least 400 U/mg. The enzyme can be used to produce
 CC (R)-alcohols by enantioselective reduction of ketones of formula
 CC R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl,
 CC aryl or arylenyl (sic) optionally substituted by halogen, NO2, OH
 CC or 1-20C alkoxy, "an optionally substituted 1-10C alkylene group,
 CC which is substituted by saturated, unsaturated or aromatic
 CC nitrogen, oxygen or sulphur heterocycles, or may be an optionally
 CC substituted polycondensed saturated and/or aromatic group" (sic) in
 CC the presence of the enzyme or cells containing it at 20-60 degrees
 CC C for 0.25-3 hours, or (S)-alcohols by incubating a racemic alcohol
 CC of formula R1-CHOH-R2 in the presence of the enzyme or cells
 CC containing it at 20-60 degrees C for 0.25-3 hours.

XX Sequence 252 AA;

Query Match 99.08; Score 1277; DB 18; Length 252;

Best Local Similarity 99.24; Pred. No. 6.5e-116;

Matches 250; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSNRLDKVAITGTLGIGLAIAATKFEVGEAKVMITDRHSDVGGEKAASVGTDPDQIOFF 60
 DB 1 MSNRLDKVAITGTLGIGLAIAATKFEVGEAKVMITDRHSDVGGEKAASVGTDPDQIOFF 60
 QY 61 QHDSSEDEGWTKLDATEKAPGVSTLVNNAGIAVNSVEETTTAEWRKLLAVNLGVFF 120
 DB 61 QHDSSEDEGWTKLDATEKAPGVSTLVNNAGIAVNSVEETTTAEWRKLLAVNLGVFF 120
 QY 121 GTRIGIORMKNGKLGASTIINNSSTEGFVGDPSLGAYNASKGAVRIMSKSAALDCKALDYD 180
 DB 121 GTRIGIORMKNGKLGASTIINNSSTEGFVGDPSLGAYNASKGAVRIMSKSAALDCKALDYD 180
 QY 181 VRVNVHPGIKTPLVDDLPAGEAMSORKTPMGHTGEPRNDIAYICVYLASNESKPTG 240
 DB 181 VRVNVHPGIKTPLVDDLPAGEAMSORKTPMGHTGEPRNDIAYICVYLASNESKPTG 240
 QY 241 SEFYVDGGYTAQ 252
 DB 241 SEFYVDGGYTAQ 252

RESULT 2

AAW23409
 ID AAW23409 standard; Protein; 251 AA.

XX AAW23409;

DT 27-MAR-1998 (first entry)

XX Lactobacillus kefir alcohol dehydrogenase.

KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.

OS Lactobacillus kefir.

XX Key Location/Qualifiers

FT MISC-difference 46 /note= "not defined in specification"
 FT MISC-difference 47 /note= "not defined in specification"
 FT MISC-difference 48 /note= "not defined in specification"
 FT MISC-difference 49 /note= "not defined in specification"
 FT MISC-difference 50 /note= "not defined in specification"
 FT MISC-difference 51 /note= "not defined in specification"
 FT MISC-difference 52 /note= "not defined in specification"
 FT MISC-difference 53 /note= "not defined in specification"

FT MISC-difference 54 /note= "not defined in specification"
 FT MISC-difference 55 /note= "not defined in specification"
 FT MISC-difference 56 /note= "not defined in specification"
 FT MISC-difference 57 /note= "not defined in specification"
 FT MISC-difference 58 /note= "not defined in specification"
 FT MISC-difference 59 /note= "not defined in specification"
 FT MISC-difference 60 /note= "not defined in specification"
 FT MISC-difference 61 /note= "not defined in specification"
 FT MISC-difference 62 /note= "not defined in specification"
 FT MISC-difference 63 /note= "not defined in specification"
 FT MISC-difference 64 /note= "not defined in specification"
 FT MISC-difference 65 /note= "not defined in specification"
 FT MISC-difference 66 /note= "not defined in specification"
 FT MISC-difference 67 /note= "not defined in specification"
 FT MISC-difference 68 /note= "not defined in specification"
 FT MISC-difference 69 /note= "not defined in specification"
 FT MISC-difference 70 /note= "not defined in specification"
 FT MISC-difference 71 /note= "not defined in specification"
 FT MISC-difference 130 /note= "not defined in specification"
 FT MISC-difference 131 /note= "not defined in specification"

XX EP796914-A2.

XX 24-SEP-1997.

XX 20-MAR-1997; 97EP-0104814.

XX 21-MAR-1996; 96DE-4010984.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Hummel W, Riebel B;

XX WPI; 1997-459831/43.

XX Lactobacillus brevis alcohol dehydrogenase - useful for production
 of optically active alcohol(s)

XX Example 8; Pages 28-30; 34pp; German.

XX The present Lactobacillus kefir alcohol dehydrogenase (ADH) was
 used in the isolation of a L. brevis ADH, which retains at least
 95% of its activity after 30 minutes at 20-60 degrees C and can be
 purified to a specific activity of at least 400 U/mg. The enzyme
 can be used to produce (R)-alcohols by enantioselective reduction
 of ketones of formula R1-CO-R2, where R1 and R2 = hydrogen (sic)
 or 1-20C alkyl, alkenyl, aryl or arylenyl (sic) optionally
 substituted by halogen, NO2, OH or 1-20C alkoxy, "an optionally
 substituted 1-10C alkylene group, which is substituted by
 saturated, unsaturated or aromatic nitrogen, oxygen or sulphur
 heterocycles, or may be an optionally substituted polycondensed
 saturated and/or aromatic group" (sic) in the presence of the

CC enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours,
CC or (S)-alcohols by incubating a racemic alcohol of formula
CC R1-CHOH-R2 in the presence of the enzyme or cells containing it at
CC 20-60 degrees C for 0.25-3 hours.
XX
SQ Sequence 251 AA;

Query Match 79.0%; Score 1019; DB 18; Length 251;
Best Local Similarity 80.5%; Pred. No. 7.8e-91;
Matches 202; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 2 SNRLDGKVAITGTGIGLATATKFEVGEKAVMTDRHSDVGEKAASVGTDPDQIQFPQ 61
DB 1 TORLKGKVAIVTGGTIGIGLATADAFVEGEKAVITIGRHADVGEKXXXXXXX 60
QY 62 HDSDSDGWTKLFDATEKAFGVPSTLVNAGIAVNSVEETTAERKLLAVNLGCVFFG 121
DB 61 XXXXXXXXXXLFDATEAFGPTVVNAGIAVNSVEDTTEERKLLSVNLGCVFFG 120
QY 122 TRLGQRMKNKGLGASIIINMSSIEGFVDPDSIGAYNASKGAVRIMSKSAALDCALKDYDV 181
DB 121 TRLGQAMKXXKGLGASIIINMSSIEGFVDPDSIGAYNASKGAVRIMSKSAALDCALKDYDV 180
QY 182 RVNTVHPGYIKTPLYDDLPAGEAMSORTKTPMGHIGEPNDIAYICVYLASHESKATGS 241
DB 181 RVNTVHPGYIKTPLYDDLPAGEAMSORTKTPMGHIGEPNDIAYICVYLASHESKATGS 240
QY 242 EFVVDGGYTAQ 252
DB 241 EFVVDGGYTAQ 251

RESULT 3
AAB49773
ID AAB49773 standard; protein; 254 AA.
XX AAB49773;
XX
DT 23-APR-2001 (first entry)
DE Protein with acetylpyridine derivative reducing action.
KW Optically-active pyridineethanol derivative; asymmetric reduction.
XX Candida maris.
XX
PN WO200105996-A1.
XX
PD 25-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-JP04237.
XX
PR 21-JUL-1999; 99JP-0206503.
XX
PA (KANF) KANEKA CORP.
XX
PI Kawano S, Horikawa M, Yasohara Y, Hasegawa J;
XX
DR WPI: 2001-159546/16.
DR N-PSDB; AAF29375; AAF29376.
XX
XX Efficient, high-yielding preparation of optically-active
PT pyridineethanol derivatives by stereoselectively reducing
PT acetylpyridine derivatives e.g. with enzyme having asymmetric reduction
PT activity, for pharmaceutical intermediates -
XX
PS Claim 14; Fig 1; 76pp; Japanese.
XX
CC This invention relates to a process for producing optically-active
CC pyridineethanol derivatives by stereoselectively reducing acetylpyridine
CC derivatives with an enzyme or enzyme source having asymmetric reduction
CC activity. The process is efficient and high yielding to give R and S
CC isomers by suitable manipulation. The method is for the preparation of

CC optically-active pyridineethanol derivatives by stereoselectively
CC reducing acetylpyridine derivatives, and also similarly for their
CC polycyclic analogues, for use as pharmaceutical and agrochemical
CC intermediates, as well as in fine chemical production. The present
CC sequence represents the amino acid sequence of the enzyme used in the
CC process which has acetylpyridine derivative reducing action.
XX
SQ Sequence 254 AA;

Query Match 35.3%; Score 456; DB 22; Length 254;
Best Local Similarity 40.2%; Pred. No. 4.1e-36;
Matches 104; Conservative 49; Mismatches 94; Indels 12; Gaps 5;

QY 1 MSNRLDGKVAITGTGIGLATATKFEVGEKAVMITD-----RHSYDGEKAASVGTGP 54
DB 1 MSYFANKVLIIVTGLSGIGLAVANKKFLQGAQKVTISDISATEKYNTVVGEFKTEGIDVK 60
QY 55 DOIQFQHDSDSDGWTKLFDATEKAFGVPSTLVNAGIAVNSVEETTAERKLLAVN 114
DB 61 N-VQYIQADASKADEAKELISLTSFAFGDLVDVCANAGIATFTQTTDISYDVMRKVTSIN 119
QY 115 LDGVVFGTRLGITORMKNKGLGASIIINMSSIEGFVDPDSIGAYNASKGAVRIMSKSAALDC 174
DB 120 LDGVFMDLKLAAQYFLSKNKPAGIYVNMGSIHYSYVAAPGLSHYGAAGKGLLTQTMALEY 179
QY 175 ALKDYDVRVNTVHPGYIKTPLYDDLPAGEAMSOR-TKTPMGHIGEPNDIAYICVYLASN 233
DB 180 AAK--GIRVNSVNPYIKTPLLDICP--KEHMDYLITQHPIGRLGKPEEIASAVAFCLSD 235
QY 234 ESKPATGSEFVVDGGYTAQ 252
DB 236 EATFINGISLLVDGGYTAR 254

RESULT 4
AAB47522
ID AAB47522 standard; Protein; 254 AA.
XX AAB47522;
XX
DT 04-DEC-2001 (first entry)
DE (R)-2-octanol dehydrogenase.
KW (R)-2-octanol dehydrogenase; ketone; alcohol; beta-NAD; co-enzyme;
KW oxidize; optical isomer; (R)-2-octanol; 4-haloacetate ester;
KW (S)-4-halo-3-hydroxybutyrate ester; HMG-CoA reductase inhibitor;
KW D-carnitine; (R)-propoxybenzene.
XX Pichia finlandica.
XX
PN WO200161014-A1.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-JP01082.
XX
PR 16-FEB-2000; 2000JP-0043506.
PR 08-DEC-2000; 2000JP-0374593.
XX
PA (DAIL) DAICEL CHEM IND LTD.
XX
PI Kudoh M, Yamamoto H;
XX
DR WPI: 2001-596701/67.
DR N-PSDB; AAB43472.
XX
PT (R)-2-octanol dehydrogenase for producing intermediates for HMG-CoA
PT reductase inhibitors or D-carnitine -
XX
PS Claim 9; Page 83-85; 97pp; Japanese.
XX
CC This sequence represents (R)-2-octanol dehydrogenase which has the

following characteristics:

CC (1) produces ketones by oxidizing alcohol using beta-NAD as a
 CC co-enzyme; and produces alcohols by reducing ketones using beta-NADH
 CC as a co-enzyme; and
 CC (2) preferentially oxidizes the optical isomer (R)-2-octanol; and
 CC reduces 4-haloacetate ester to produce (S)-4-halo-3-
 CC hydroxybutyrate ester.
 CC (S)-4-halo-3-hydroxybutyrate esters are useful as intermediates
 CC for HMG-CoA reductase inhibitors or D-carnitine. (R)-propoxybenzene
 CC derivatives are particularly useful as intermediates for optical
 CC isomers of ofloxane (S)-(-)-9-fluoro-3-methyl-10-(4-methyl-1-
 CC piperazinyl)-7-oxo-2,3-dihydro-7H-pyrido(1,2,3-de)(1,4) benzoxadin-
 CC 6-carboxylic acid).

XX SQ Sequence 254 AA;
 Query Match 34.9%; Score 450; DB 22; Length 254;
 Best Local Similarity 39.0%; Pred. No. 1.6e-35;
 Matches 101; Conservative 46; Mismatches 100; Indels 12; Gaps 5;
 QY 1 MSNRLDGKVAITGTLGIGLAIAATKFEVGEAKVMTD-----RHSDVGEAKASVGTG 54
 DB 1 MSYFNHKNVAVVTGALSGISLVAKKFLQLGAKVTISDVSGEKYKVTETVVALKAQNLNT- 59
 QY 55 DOIQFFHDSDEDEGWTKLFDATEKAGPVPSTLVNNAIAVNSVEETTTAEWRKLLAVN 114
 DB 60 DNLHYQADSSKEEDNKKLISETLATGGLDIVCANAGIKGFAPTHETPTDVKKVIYAVN 119
 QY 115 LDGVFFETRLGIQRMKNKGLGASINSSIEGFVGDPSLGAYNASKGAVRTKSKAALDC 174
 DB 120 LNVFLDLKLAINYWLEKSRPGVIVNMGSHVFAAFGLAHYGAAGVKLTOTLALAY 179
 QY 175 ALKDYVRVNTVHPGYIKTPLVDLPGAEAEAMSQRTKT-PMGHIGEPNDIAYICVILASN 233
 DB 180 A--SHGIRVANSVNPYISTPLIDEVP--KERLDKLVSLHPIGRLGRPEEVADAVFLCSQ 235
 QY 234 ESKFATGSEFFVDDGYTAQ 252
 DB 236 EATFINGVSLPVDGGYTAQ 254

RESULT 5

AAV56815
 ID AAY56815 standard; Protein; 258 AA.

XX AAY56815;

XX 31-MAR-2000 (first entry)

XX Bacillus D-arabinitol dehydrogenase.

XX D-arabinitol dehydrogenase; clinical diagnosis; mycosis.

XX Bacillus sp.

XX JP11332569-A.

XX 07-DEC-1999.

XX 26-MAY-1998; 98JP-0143637.

XX 26-MAY-1998; 98JP-0143637.

XX (IKED-) IKEDA SHOKKEN KK.

XX (NIPK) NIPPON KAYAKU KK.

XX WPI: 2000-091353/08.

XX N-PSDB; AA246762, AA246763.

XX Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase -

PT useful as a clinical diagnosing agent for mycosis

XX Claim 1; Page 10-11; 14pp; Japanese.

XX

CC The invention relates to gene encoding D-arabinitol dehydrogenase,
 CC isolated from *Bacillus* sp. IKD-5A868 strain. The protein can be expressed
 CC by standard recombinant methodologies. D-arabinitol dehydrogenase is used
 CC as a clinical diagnosing agent for mycosis. The present sequence
 CC represents the D-arabinitol dehydrogenase enzyme.

XX SQ Sequence 258 AA;

Query Match 31.0%; Score 400; DB 21; Length 258;

Best Local Similarity 39.4%; Pred. No. 1.2e-30;

Matches 100; Conservative 41; Mismatches 101; Indels 12; Gaps 7;

QY 4 RLDGKVAITGTLGIGLAIAATKFEVGEAKVMTDRHSDVGEAKA--KSVGTDPDQIOFF 60
 DB 8 RLDGRVITVTCAGHGLGRAMALALAQAAGSHIVADIRADEAQAENIRSCGV--EATV 65
 QY 61 QHDSDEGWTKLFDATEKAFGPVSTLVNNAIAVNSVEETTTAEWRKLLAVNLDGVFF 120
 DB 66 QTDVTDEAQAVALIRQVEEQYGRDLVLVNNAGIVHKDRAELPYETWNRVNNVNLNVFL 125
 QY 121 GTRLGIQRMKNKGLGASIIINSSIEG-FVGDPS-LGAYNASKGAVRIMSKSAALDCAL 178
 DB 126 MSKAAGKVMTIRQKG-SIINISSMSGLIVNTPQPAAYNVSKAGVIMLTSLASEWA--P 182
 QY 179 YDVRVNTVHPGYIKTPLVDD--LPGAEAMSQRTKTPMGHIGEPNDIAYICVILASN 236
 DB 183 HGVVNTIAGYMKTKTEPYFAAGGEMIDKWLAMPGRPGVPHELGGIAYILASOASS 242
 QY 237 FATGSEFFVDDGYT 250
 DB 243 FATGGVETIDGGYT 256

RESULT 6

AAU37095

ID AAU37095 standard; Protein; 272 AA.

XX AAU37095;

XX 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #1265.

XX Antisense; prokaryotic cellular proliferation protein;

XX antibiotic; antibacterial; drug design.

XX Staphylococcus aureus.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-0509180.

XX 21-MAR-2000; 2000US-191078P.

XX 23-MAY-2000; 2000US-206848P.

XX 26-MAY-2000; 2000US-207727P.

XX 23-OCT-2000; 2000US-242578P.

XX 27-NOV-2000; 2000US-253625P.

XX 22-DEC-2000; 2000US-257931P.

XX 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI: 2001-611495/70.

XX N-PSDB; AAS54954.

XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -

XX PS Example 3; Seq ID No 12688; 51pp; English.
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the
XX CC genes, their use in the discovery of novel antibiotics, the essential
XX CC genes themselves and the encoded proteins. The prokaryotes used are
XX CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX CC invention is also useful for the identification of potential new targets
XX CC for antibiotic development. The antisense nucleic acids can also be used
XX CC to identify proteins used in proliferation, to express these proteins,
XX CC and to obtain antibodies capable of binding to the expressed proteins.
XX CC The proteins can be used to screen compounds in rational drug discovery
XX CC programmes. The antisense nucleic acid sequence is also useful to screen
XX CC for homologous nucleic acids which are required for cell proliferation in
XX CC a wide variety of organisms. The present sequence represents an
XX CC essential prokaryotic cellular proliferation protein.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 272 AA;

Query Match 28.6%; Score 369; DB 22; Length 272;
Best Local Similarity 35.8%; Pred. No. 1.3e-27;
Matches 92; Conservative 42; Mismatches 109; Indels 14; Gaps 6;
QY 4 RLDGVAITGCTGLGIAIAIKFVEEGAKYMITDRHSDVGEKAASVGTDPDQIOFFQHD 63
DB 3 RLENKVVAVTGTAGTIGQASATAQAEGAYVLAVDAEAVSETYDKIKNSGDKAKAYVD 62
QY 64 SDEDEGWTKLFDATKAFGPVSTLVNNAAGI--AVNKSVEETTTAEWRKILAVNLDGVFFG 121
DB 63 INAEQIDNFASEIREQFGHVDVLENNAGVDNAAGR-THEPTDYDKIMVDMRGTFM 121
QY 122 TRLGTRMKNKGLGASINMSIEGFVGDPSLGAYNASKGAVRIMSKAALDKALDYDV 181
DB 122 TKMLPLMTK--GGSIVNTSFSGQAADLYRSGYNAAGAVINFTKSIATYEG-RD-GI 177
QY 182 RVNTHVPGYIKTPLVDLDPGAE-----AMSQRTKTPMGHIGEPNDIAYICVYLASNE 234
DB 178 RANAAPGTIETPLVDKLTGTSEDGKAFRENQKMTPLRLGRPEVGLVWFLASDE 237
QY 235 SKFATGSEFVVDGGYTA 251
DB 238 SSFITEGIRIDGGYMA 254

RESULT 7
AAR27757
ID AAR27757 standard; protein; 261 AA.
AC AAR27757;
DT 11-MAR-1993 (first entry)
DE Glucose dehydrogenase.
KW GDH; mutant; recombinant; mass production; tetramer; thermostable.
OS Bacillus megaterium.
PH Key Location/Qualifiers
FT Misc-difference 96 /note= "site of Glu->Val or Lys mutation"
FT Misc-difference 252 /note= "site of Gln->Leu mutation"
FT Misc-difference 253 /note= "site of Tyr->Glu mutation"
FT Misc-difference 22 /label= Ser, Ala

FT Misc-difference 43 /label= Asp, Glu
FT Misc-difference 79 /label= Ala, Ser
FT Misc-difference 95 /label= Leu, Met
XX JP04258293-A.
XX 14-SEP-1992.
XX 13-FEB-1991; 91JP-0106927.
XX 13-FEB-1991; 91JP-0106927.
XX (AMANO) AMANO PHARM KK.
XX WPI; 1992-354684/43.
XX Glucose dehydrogenase prep. using transformed recombinant DNA
XX from Bacillus megaterium - has specified transformations giving
XX glucose dehydrogenase-expressing vector, introduced into E.coli.
XX for culture
XX Claim 1; Page 8; 12pp; Japanese.
XX The glucose dehydrogenase enzyme is encoded by a recombinant DNA
XX clone from Bacillus megaterium. The DNA sequence may be mutated by
XX site directed mutagenesis to introduce mutations to the protein
XX sequence (see feature table). The DNA may be used to transform E.
XX coli cells, and transformants may be cultured to mass produce GDH.
XX The mutant GDH is not influenced by ion strength, exists as a
XX tetramer and is thermostable.
XX Sequence 261 AA;

Query Match 28.5%; Score 367.5; DB 13; Length 261;
Best Local Similarity 33.3%; Pred. No. 1.7e-27;
Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;
QY 1 MSNRDLGKVAITGCTGLGIAIAIKFVEEGAKYMITDRHSDVGEKAA----KSVGTDPQ 56
DB 1 MYKLEGVAVTGTSTGLGKXMAIRFATEKAKVYVNVYRSEKXEVLEEKVKG--GE 58
QY 57 IOFFHDSDEGWTKLFDATKAFGPVSTLVNNAAGIANKSVETTTAEWRKILAVNLD 116
DB 59 AIYAKGDTVESDVINLVQSKIKEFGKLDVMINNAGXENPVSSHMSLSDNKVIDTNLT 118
QY 117 GVFFCTRLGIQRMKNKGLGASINMSIEGFVGDPSLGAYNASKGAVRIMSKAALDCAL 176
DB 119 GAFLGSRRAIKYFVENDIKGTVINNMSVHEKIPTPLFVHYAASKGKMLTETLALAYAP 178
QY 177 KDYDVRVNVTHPGYIKTPL-VDDLPGAEAMSQRTKTPMGHIGEPNDIAYICVYLASNE 235
DB 179 K--GIRVNNIGPGAINTPINAIEKFADEQADVESNIPMGYIGEPEETAATAVLAASPA 236
QY 236 KFATGSEFVVDGGYT 250
DB 237 SYVTGITLEFDGGMT 251

RESULT 8
AAR04044
ID AAR04044 standard; protein; 261 AA.
XX AAR04044;
XX 02-MAR-1993 (first entry)
XX Glucose dehydrogenase.
XX GDH; vector; E. coli; enzyme; assay; food.
XX

```

OS  Bacillus megaterium.
XX
FH  Key Location/Qualifiers
FT  Misc-difference 22 /label= SER, ALA
FT  Misc-difference 43 /label= ASP, GLU
FT  Misc-difference 79 /label= ALA, SER
FT  Misc-difference 95 /label= LEU, MET
XX
PN  JP02072878-A.
XX
PD  13-MAR-1990.
XX
PP  06-SEP-1988; 88JP-0223343.
XX
PR  06-SEP-1988; 88JP-0223343.
XX
PA  (AMAN ) AMANO PHARM KK.
XX
DR  WPI; 1990-121044/16.
XX
XX  Glucose dehydrogenase prodn. from Bacillus megaterium - by
PT  culturing recombinant DNA-contg. transformants in nutrient
PT  culture medium, used in food industry
XX
PS  Claim 1; : 12pp; Japanese.
XX
CC  DNA encoding glucose dehydrogenase (GDH) derived from B. megaterium
CC  encodes the amino acid sequence below. The DNA may be integrated
CC  into a vector for replication in E. coli. A large amt. of GDH may
CC  be produced at low cost. The GDH is used in clinical laboratory
CC  tests in the food industry in enzymic assays for glucose
CC  determination.
XX
SQ  Sequence 261 AA;

Query Match 28.3%; Score 364.5; DB 11; Length 261;
Best Local Similarity 33.3%; Pred. No. 3.4e-27;
Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;

QY  1 MSNRLDGKVAITGGTGLGIGLAIAATKFEVGAKVMTDRHSDVGEKAA----KSVGTPDQ 56
DB  1 MYKDLGKVVVITGSGTGLGKXMAIRFATEKAKVVVYRSKEXEANSVLEEIKVKG--GE 58
QY  57 IQFFHDSDEDEGWTKLFDATKAFGCPVSTLVNAGIANKSVETTTAEWRKLLAVNLD 116
DB  59 ATAVKGDVTVESDVINLVOSKIKFEKGLDVMINNAGXENPVSSHMSLSDNKVIDTNLT 118
QY  117 GVFFGTRLGIQRMKNKGLGASINMSIEGFVGDPSLGAYNASKGAVRTMKSAAALDCL 176
DB  119 GAFLSREAIKFVENDIGTVINMSVHEKIPWPLFVHYAASKGGMKLTETLALEYAP 178
QY  177 KYDVRVNTVHPGYIKTPL-VDDLPGAEAMSORTKTPMGHICEPNNDIAYICVYLASNES 235
DB  179 K-GIRVNNIGPGAINTPINAERFADPQERADVESNIPMGYIGEPEIAAFAVAWLASSEA 236
QY  236 KTAGSEFVVDGGYT 250
DB  237 SYVTGITLFDAGGMT 251

RESULT 9
AAR24018
ID  AAR24018 standard; Protein; 261 AA.
AC  AAR24018;
XX
XX  27-NOV-1992 (first entry)
XX
DE  Thermostable glucose dehydrogenase from Bacillus megaterium.

Thermostable; increased heat stability; GDH.
Bacillus megaterium.
Key Location/Qualifiers
Misc-difference 22 /label= Ser, Ala
Misc-difference 43 /label= Asp, Glu
Misc-difference 79 /label= Ala, Ser
Misc-difference 95 /label= Leu, Met
/note= "together with residues 252,253 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
Misc-difference 252 /note= "together with residues 96,253 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
Misc-difference 253 /note= "together with residues 96,252 may be replaced by a thermostability-conferring amino acid provided that taken together they are not Glu, Gln, and Tyr respectively"
US5114853-A.
19-MAY-1992.
22-SEP-1989; 89US-0410844.
22-SEP-1988; 88JP-0237699.
(AMAN ) AMANO PHARM KK.
Makino Y, Negoro S, Okada H, Urabe I;
WPI; 1992-192176/23.
DNA contg. glucose dehydrogenase gene of Bacillus megaterium - used to express heat stable protein in Escherichia coli, e.g. with glutamine 96 replaced by alanine
Claim 1; Column 13; 10pp; English.
A DNA library was prepared in E. coli C600, and screened with probe AQ29704, resulting in 3 positive colonies. These were cultured, and plasmid DNA prepared from them and cut with EcoRI and SalI. The probe AQ29704 was then used to probe a PAGE gel and found to strongly hybridise with a 3.6kb fragment. The 3 colonies were all thus found to have the same plasmid, and this was named pGDAL. pGDAL was cut with EcoRI and Sau3AI, and a 930bp fragment produced and sequenced, and was found to encode the sequence given. pGDAL was then cut with EcoRI and PvuII and a 1.5kb fragment isolated. This was then cloned into expression vector pKK223-3 and transformed into E. coli JM105.
Query Match 28.3%; Score 364.5; DB 13; Length 261;
Best Local Similarity 33.3%; Pred. No. 3.4e-27;
Matches 85; Conservative 49; Mismatches 112; Indels 9; Gaps 4;

QY  1 MSNRLDGKVAITGGTGLGIGLAIAATKFEVGAKVMTDRHSDVGEKAA----KSVGTPDQ 56
DB  1 MYKDLGKVVVITGSGTGLGKXMAIRFATEKAKVVVYRSKEXEANSVLEEIKVKG--GE 58
QY  57 IQFFHDSDEDEGWTKLFDATKAFGCPVSTLVNAGIANKSVETTTAEWRKLLAVNLD 116

```

Db 59 ATAVGQDVTVESVNLVOSXIKFEKLDVMNNAGXENPVSSHESLSDMKNKVIDNTLT 118
QY 117 GVFFCTRLGIORMKNGKLGASIIINSSIEGFVCDPSLGAYNASKGAVRIMSKSAALDCAL 176
Db 119 GAFLGSREAIKVFVENDIKGTVINSSVHEKIPWPLFVHYAASKGKMLTETLALEYAP 178
QY 177 KOYDVVNVTVHPGYIKTPL-VDDLPGAEEAMSORTKTPMGHIGEPNDIAIYICVYLASNES 235
Db 179 K-GIRVNNIGCAINTPINAEEKFADPQERADVESIMPYIGEPEIEIAVAANWLASSEA 236
QY 236 KEATGSEFVVDGGYT 250
Db 237 SYVTGTLTADGGMT 251

RESULT 10
AAU34193
ID AAU34193 standard; Protein; 251 AA.
XX AAU34193;
XX
DT 14-FEB-2002 (first entry)
XX
DE Staphylococcus aureus cellular proliferation protein #469.
XX
KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PP 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS52052.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3; Seq ID No 5689; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 251 AA;

Query Match 28.2%; Score 364; DB 22; Length 251;
Best Local Similarity 35.5%; Pred. No. 3 6e-27;
Matches 91; Conservative 42; Mismatches 109; Indels 14; Gaps 6;

QY 5 LDGKVAITGGTGLGIAIATKFEVGAQVMTDRHSVDYGEKAASVGTPTDQIQFQHDS 64
Db 1 LENKAVVTGASTGICQASAIALAOEGAYFLAVIAEAVSETVDKIKNSDKAKAVVVDI 60
QY 65 SDEGWTKLFDATKAFGVPSTLVNNAGI--AVNKSVEETTTAEWRKLLAYNLGDGVFFGT 122
Db 61 ASEQQIDNFASEIREFQGHVDVLFNAGYDVAAGR-IHEYPTDVKIMNVDMRGTFMT 119
QY 123 RLGIQRMKNKGLGASIIINSSIEGFVCDPSLGAYNASKGAVRIMSKSAALDCALKDYDVR 182
Db 120 KMLPLMWTK--GGSIWTSFSGQAADLYRSGYNAKAGAVINFTKSIATIEYG-RD-GIR 175
QY 183 VNTVHPGYIKTPLVDDLPGAEE-----AMSOQRTKTPMGHIGEPNDIAIYICVYLASNES 235
Db 176 ANAIAPGTIETPLVDKLTGCTSEDKEGKAPRENQKWTPLGLRGKPEVGKLVVFLASDES 235
QY 236 KEATGSEFVVDGGYT 251
Db 236 SEITGETIRIDGGVMA 251

RESULT 11
RAB10740
ID AAB10740 standard; Protein; 272 AA.
XX
AC AAB10740;
XX
DT 26-JAN-2001 (first entry)
XX
DE B. megaterium glucose dehydrogenase GlcDH protein.
XX
KW Glucose dehydrogenase; GlcDH; fusion protein; detection.
XX
OS Bacillus megaterium.
XX
PN WO200049039-A2.
XX
PD 24-AUG-2000.
XX
PP 08-FEB-2000; 2000WO-EP00978.
XX
PR 19-FEB-1999; 99DE-1006920.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Linxweiler W, Burger C, Poeschke O, Hofmann U, Wolf A;
XX
DR WPI; 2000-558290/51.
DR N-PSDB; AAA97948.
XX
XX Glucose dehydrogenase fusion proteins, useful in expression systems for
PT quick detection of foreign proteins by gel electrophoresis -
XX
XX Disclosure; Page 54-55; 63pp; German.
XX
XX This invention describes a novel recombinant fusion protein (A)
CC comprising at least a first and a second amino acid sequence,
CC characterized in that the first sequence has the biological activity of
CC a glucose dehydrogenase. Glucose dehydrogenase is useful as a detector
CC protein (in a detection system) for any type of recombinant
CC protein/polypeptide in a fusion protein. Glucose dehydrogenase can be
CC used to detect protein-protein interactions, where it corresponds to a

CC partner of a recombinant protein/polypeptide. Expression vectors encoding
 CC the fusion proteins are useful to optimize the expression of the
 CC recombinant protein/polypeptide in a recombinant production method. The
 CC host cell is also useful for recombinant production of the
 CC protein/polypeptide. The fusion proteins containing glucose dehydrogenase
 CC can be quickly detected in SDS-PAGE gels. This sequence represents the
 CC Bacillus megaterium glucose dehydrogenase GlcDH which is used in the
 CC construction of fusion proteins as described in the method of the
 CC invention.
 XX
 SQ Sequence 272 AA;

Query Match 28.2%; Score 363.5; DB 21; Length 272;
 Best Local Similarity 31.5%; Pred. No. 4.5e-27;
 Matches 82; Conservative 51; Mismatches 108; Indels 19; Gaps 4;
 QY 1 MSNRLDGKVAITGTLGIGLAIAIKFVEEGAKVMIT-----DRHSDVGEKAASV 51
 DB 1 MYTDLKRVVITGSGTGLGRAMAVRFGQEEAKVYINYNNEEALDAKKEVEEAGGQAI 60
 QY 52 GTPDQIOFFQHDSDSDGWTKLDATEKAFGVPSTLVNNAIGAVNKSVEETTTAEWRKLL 111
 DB 61 -----IVQGDVTKEDVNLVQTAKFETLDVMINNAGVENPVPFSLDLNWNKVI 113
 QY 112 AVNLDGVFFGTRIGIORMKNGKLGASIIINSSIEGFVDPDPSLGAYNASKGAVRIMSKSAA 171
 DB 114 DTNLTGAFLSREAIAKYFVENDIKGNVINSSVHEMIPWLFVHYAASKGKMLTETLA 173
 QY 172 LDCALKDYDVRVNTVHFGYIKTPL-VDDLPAGEEAMSORTKTPMGHIGEPNDIAYICVYL 230
 DB 174 LEYAPK--GIRVNNIGPGAMNTPINAEKFADEQRADEVSMIPMGYIGKPEEVAVA AFL 231
 QY 231 ASNESKATGSEFVVDDGYT 250
 DB 232 ASSQASVTGTTLFADGGMT 251

RESULT 12

AA010741
 ID AAB10741 standard; Protein; 340 AA.
 AC AAB10741;
 XX
 XX 26-JAN-2001 (first entry)
 DT
 XX H. ghillani/B. megaterium fusion protein Tridegin/GlcDH.
 XX Glucose dehydrogenase; GlcDH; fusion protein; detection; tridegin.
 XX
 OS Heamenteria ghillani.
 OS Bacillus megaterium.
 XX
 XX Key Location/Qualifiers
 FT Protein 1..68
 FT /note- "tridegin protein"
 FT Protein 69..340
 FT /note- "GlcDH"
 XX
 XX W0200049039-A2.
 XX
 XX 24-AUG-2000.
 XX
 XX 08-FEB-2000; 2000WO-EP00978.
 XX
 XX 19-FEB-1999; 99DE-1006920.
 XX
 XX (MERE) MERCK PATENT GMBH.
 XX
 XX Linxweiler W, Burger C, Poeschke O, Hofmann U, Wolf A;
 XX WPI: 2000-558290/51.
 XX N-PSDB; AAA97949.
 XX

PT Glucose dehydrogenase fusion proteins, useful in expression systems for
 PT quick detection of foreign proteins by gel electrophoresis
 XX
 XX Disclosure; Page 59-60; 63pp; German.

CC This invention describes a novel recombinant fusion protein (A)
 CC comprising at least a first and a second amino acid sequence,
 CC characterized in that the first sequence has the biological activity of
 CC a glucose dehydrogenase. Glucose dehydrogenase is useful as a detector
 CC protein (in a detection system) for any type of recombinant
 CC protein/polypeptide in a fusion protein. Glucose dehydrogenase can be
 CC used to detect protein-protein interactions, where it corresponds to a
 CC partner of a recombinant protein/polypeptide. Expression vectors encoding
 CC the fusion proteins are useful to optimize the expression of the
 CC recombinant protein/polypeptide in a recombinant production method. The
 CC host cell is also useful for recombinant production of the
 CC protein/polypeptide. The fusion proteins containing glucose dehydrogenase
 CC can be quickly detected in SDS-PAGE gels. This sequence represents a
 CC fusion protein constructed from the H. ghillani tridegin protein and the
 CC Bacillus megaterium glucose dehydrogenase GlcDH which is described in the
 CC method of the invention.
 XX

SQ Sequence 340 AA;

Query Match 28.2%; Score 363.5; DB 21; Length 340;
 Best Local Similarity 31.5%; Pred. No. 6.1e-27;
 Matches 82; Conservative 51; Mismatches 108; Indels 19; Gaps 4;
 QY 1 MSNRLDGKVAITGTLGIGLAIAIKFVEEGAKVMIT-----DRHSDVGEKAASV 51
 DB 69 MYTDLKRVVITGSGTGLGRAMAVRFGQEEAKVYINYNNEEALDAKKEVEEAGGQAI 128
 QY 52 GTPDQIOFFQHDSDSDGWTKLDATEKAFGVPSTLVNNAIGAVNKSVEETTTAEWRKLL 111
 DB 129 -----IVQGDVTKEDVNLVQTAKFETLDVMINNAGVENPVPFSLDLNWNKVI 181
 QY 112 AVNLDGVFFGTRIGIORMKNGKLGASIIINSSIEGFVDPDPSLGAYNASKGAVRIMSKSAA 171
 DB 182 DTNLTGAFLSREAIAKYFVENDIKGNVINSSVHEMIPWLFVHYAASKGKMLTETLA 241
 QY 172 LDCALKDYDVRVNTVHFGYIKTPL-VDDLPAGEEAMSORTKTPMGHIGEPNDIAYICVYL 230
 DB 242 LEYAPK--GIRVNNIGPGAMNTPINAEKFADEQRADEVSMIPMGYIGKPEEVAVA AFL 299
 QY 231 ASNESKATGSEFVVDDGYT 250
 DB 300 ASSQASVTGTTLFADGGMT 319

RESULT 13

AA03846
 ID AAR03846 standard; protein; 261 AA.
 AC AAR03846;
 XX
 XX 09-AUG-1990 (first entry)
 DT
 XX Modified glucose dehydrogenase gene of Bacillus megaterium.
 DE
 XX Glucose dehydrogenase; Bacillus megaterium; heat stability;
 KW glucose assay; ss.
 XX
 XX Bacillus megaterium.
 XX
 XX DE3931716-A.
 XX
 XX 29-SEP-1988.
 XX
 XX 22-SEP-1989; 89DE-3931716.
 XX
 XX 22-SEP-1988; 88JP-0237699.
 XX
 XX (AWAN) AMANO PHARM KK.

XX PI Makino YS, Negoro S, Urabe IA, Okada HT;
XX DR WPI; 1990-100507/14.
XX PT New DNA encoding modified forms of glucose dehydrogenase -
XX PT from Bacillus megaterium, having specific amino acid
XX PT replacements, with higher heat stability.
XX PS Claim 1; Page 13; 16pp; German.
XX CC The normal Glu-96 residue is replaced by Lys, Gly or Ala.Gln-252 by
XX CC Leu or Tyr-253 by Cys. Ser-22 residue can also be Ala, Asp-43 can be
XX CC Glu, Ala-79 can be Ser and Leu-95 can be Met.E.coli containing this
XX CC sequence will produce a form of GDH with improved heat stability. the
XX CC enzymes are useful for glucose assay and can be produced at low costs
XX CC or in large amounts.
XX CC See also RAQ03772.
XX SQ Sequence 261 AA;
Query Match 27.9%; Score 360.5; DB 11; Length 261;
Best Local Similarity 33.6%; Pred. No. 8.2e-27;
Matches 86; Conservative 49; Mismatches 110; Indels 11; Gaps 4;
QY 1 MSNRLDGKVAITGGTGLGIGLAIAIKFVEEGAKVMT-----DRHSDVGEKAASVGTDP 55
DB 1 MYKDLGKVVVITGGTGLGIGLAIAIKFVEEGAKVMT-----DRHSDVGEKAASVGTDP 60
QY 56 QIOFQHDSSDEGWTKLFDATKAFPGVSTLVNNAIAVNSVETTTAEWRKLL 115
DB 61 AV---KGVTVESDVINLVQSAIKFEGKLDVMINNAGLNPSVSHMSLSDNKVIDTNL 117
QY 116 DGVEFFTRIGIORMKNGKLGASIIINSSIEGFGVDPGLGAYNASKGAVRIMSKSAALDCA 175
DB 118 WGAFLGSRRAIKFYFVENDIKGVINSSVHEKIPWFLFVHYAASKGKMLMHWENLALEYA 177
QY 176 LKDYDVRVNTVHPGYIKTPL-VDDLPAGEAAMSQRTKTPMGHIGEPNDIAYICVILASNE 234
DB 178 PK--GIRVNNIGPGAINTPINAEKPADPQERADVESMIPMGYIGEPEETAAVAANLASSE 235
QY 235 SKFATGSEFVVDGGYT 250
DB 236 ASYVTGTLTILFADGGMT 251
RESULT 14
AAR27756
ID AAR27756 standard; protein; 261 AA.
XX AC AAR27756;
XX DT 11-MAR-1993 (first entry)
XX DE NAD affinity glucose dehydrogenase.
XX KW GDH; glucose; recombinant.
XX OS Bacillus megaterium.
XX FH Key Location/Qualifiers
FT Misc-difference 96
FT /label= Glu, Leu
FT Misc-difference 258
FT /label= Thr, Ala
XX PN JP04258289-A.
XX PD 14-SEP-1992.
XX PF 13-FEB-1991; 91JP-0187085.
XX PR 13-FEB-1991; 91JP-0187085.

XX PA (AMAN) AMANO PHARM KK.
XX DR WPI; 1992-354681/43.
XX DR N-PSDB; AAQ29486.
XX PT New NAD affinity glucose dehydrogenase - obtd. from Bacillus
XX PT megaterium
XX PS Disclosure; Page 5; 8pp; Japanese.
XX CC The Bacillus megaterium derived NAD affinity glucose dehydrogenase
XX CC may be prepd. recombinantly by inserting its gene into a vector and
XX CC using this to transform E. coli. The enzyme may be used in a kit to
XX CC determine the amt. of glucose in a sample.
XX SQ Sequence 261 AA;
Query Match 27.9%; Score 359.5; DB 13; Length 261;
Best Local Similarity 31.9%; Pred. No. 1e-26;
Matches 83; Conservative 48; Mismatches 110; Indels 19; Gaps 4;
QY 1 MSNRLDGKVAITGGTGLGIGLAIAIKFVEEGAKVMT-----DRHSDVGEKAASV 51
DB 1 MYTDLKDKVVVITGGTGLGIGLAIAIKFVEEGAKVMT-----DRHSDVGEKAASV 60
QY 52 GTPDQIQFQHDSSDEGWTKLFDATKAFPGVSTLVNNAIAVNSVETTTAEWRKLL 111
DB 61 -----IVQGDVTKEDVVNLVQTAKEFGTLDVMINNAGVENPVPSELSLDNNKVI 113
QY 112 AVNLGCVFFTRIGIORMKNGKLGASIIINSSIEGFGVDPGLGAYNASKGAVRIMSKSAA 171
DB 114 DTNLTCGAFGLSREAIFYFVENDIKGVINSSVHEMIPWFLFVHYAASKGKMXMTETLA 173
QY 172 LDCALKDYDVNTVHPGYIKTPL-VDDLPAGEAAMSQRTKTPMGHIGEPNDIAYICVYL 230
DB 174 LSYAPK--GIRVNNIGPGAINTPINAEKPADPQERADVESMIPMGYIGRPEEVAANAFL 231
QY 231 ASNESKFATGSEFVVDGGYT 250
DB 232 ASSEASVYTGTLFADGGMT 251
RESULT 15
AAP80590
ID AAP80590 standard; protein; 261 AA.
XX AC AAP80590;
XX DT 14-SEP-1990 (first entry)
XX DE Sequence of glucose dehydrogenase (GD) from Bacillus megaterium as
XX DE encoded on plasmid pJH11.
XX KW Bacillus megaterium; non-pathogenic; glucose dehydrogenase;
XX KW plasmid pSAC4 (DSM 4053P); B. megaterium strain M1296/PSAC2 (DSM 4050);
XX KW B. megaterium strain M1296/PSAC2 (DSM 4048); high protein yields;
XX KW B. megaterium strain M1296/PSAC4 (DSM 4049); plasmid pUH111.
XX OS Bacillus megaterium.
XX PN EP285949-A.
XX PD 12-OCT-1988.
XX PF 28-MAR-1988; 88EP-0104953.
XX PR 08-APR-1987; 87DE-3711883.
XX PA (MERE) MERCK PATENT GMBH.
XX PI Ebeling W, Heilmann HJ, Meinhardt F;

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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:40 ; Search time 32 Seconds

(without alignments)
874.706 Million cell updates/sec

Title: US-09-910-033a-2

Perfect score: 252

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	71.0	252	18 AAW23407	Lactobacillus brev
2	47	18.7	251	18 AAW23409	Lactobacillus kefi
3	36	14.3	50	20 AAY30523	L. brevis ADH N-te
4	36	14.3	50	20 AAY33419	L. brevis wild-typ
5	28	11.1	50	20 AAY33424	L. brevis ADH pept
6	27	10.7	50	20 AAY33420	L. brevis ADH pept
7	27	10.7	50	20 AAY33421	L. brevis ADH pept
8	27	10.7	50	20 AAY33422	L. brevis ADH pept
9	27	10.7	50	20 AAY33423	L. brevis ADH pept
10	25	9.9	38	18 AAW23408	Lactobacillus kefi
11	20	7.9	34	20 AAY33413	L. brevis NADP-dep

12	8	3.2	120	22 ABG07478	Novel human diagno
13	8	3.2	120	22 ABB40547	Peptide #8053 enco
14	8	3.2	120	22 AAW74176	Human bone marrow
15	8	3.2	136	22 AAU55352	Propionibacterium
16	8	3.2	241	22 AAB70963	S. spinosa protein
17	8	3.2	254	22 AAB49773	Protein with acety
18	8	3.2	254	22 AAB47522	(R)-2-octanol dehy
19	8	3.2	255	20 AAY39316	ORF115 protein inv
20	8	3.2	258	22 AAG92682	C glutamicum prote
21	8	3.2	258	22 AAB79361	Corynebacterium gl
22	8	3.2	272	21 AAG09589	Arabidopsis thalia
23	8	3.2	272	21 AAY77928	A. thaliana enviro
24	8	3.2	275	21 AAG09588	Arabidopsis thalia
25	8	3.2	277	19 AAW51011	Human liver carbon
26	8	3.2	317	21 AAY50903	Tomato nicotinamin
27	8	3.2	336	16 AAW06488	Maize ts2 sequence
28	8	3.2	377	21 AAG06248	Arabidopsis thalia
29	8	3.2	397	21 AAG06247	Arabidopsis thalia
30	8	3.2	485	15 AAR47812	Sequence of amino
31	8	3.2	485	21 AAG06246	Arabidopsis thalia
32	8	3.2	559	22 AAG07374	Novel human diagno
33	7	2.8	15	22 AAG67050	Human proton trans
34	7	2.8	33	21 AAY67477	S. clava antimicro
35	7	2.8	33	21 AAY67479	S. clava antimicro
36	7	2.8	34	22 AAB51232	E. coli AMP gene S
37	7	2.8	123	22 ABB40180	Peptide #7686 enco
38	7	2.8	123	22 AAM60948	Human brain expres
39	7	2.8	123	22 AAW73641	Human bone marrow
40	7	2.8	123	22 AAG33832	Peptide #7869 enco
41	7	2.8	127	18 AAY11213	S. pneumoniae 3-ox
42	7	2.8	132	21 AAY52575	Amino acid sequenc
43	7	2.8	133	22 AAG82489	S. epidermidis ope
44	7	2.8	140	21 ABA41413	Human ORFX ORF1177
45	7	2.8	171	22 AAG82281	S. epidermidis ope

ALIGNMENTS

RESULT 1	
AAW23407	
ID AAW23407 standard; Protein; 252 AA.	
XX	
AC AAW23407;	
XX	
DT 27-MAR-1998 (first entry)	
XX	
DE Lactobacillus brevis alcohol dehydrogenase.	
XX	
KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.	
XX	
OS Lactobacillus brevis.	
XX	
PN EP796914-A2.	
XX	
PD 24-SEP-1997.	
XX	
PF 20-MAR-1997; 97EP-0104814.	
XX	
PR 21-MAR-1996; 96DE-4010984.	
XX	
PA (BOEF) BOEHRINGER MANNHEIM GMBH.	
XX	
PI Hummel W, Riebel B;	
XX	
DR WPI; 1997-459831/43.	
XX	
DR N-PSDB; AAT73132.	
XX	
PT Lactobacillus brevis alcohol dehydrogenase - useful for production	
XX	
PS of optically active alcohol(s)	
XX	
PS Claim 8; Pages 24-26; 34pp; German.	

The present sequence is a *Lactobacillus brevis* alcohol dehydrogenase, which retains at least 95% of its activity after 30 minutes at 20-60 degrees C and can be purified to a specific activity of at least 400 U/mg. The enzyme can be used to produce (R)-alcohols by enantioselective reduction of ketones of formula R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl, aryl or arylenyl (sic) optionally substituted by halogen, NO2, OH or 1-20C alkoxy, "an optionally substituted 1-10C alkylene group, which is substituted by saturated, unsaturated or aromatic heterocycles, or may be an optionally substituted polycondensed saturated and/or aromatic group" (sic) in the presence of the enzyme or cells containing it at 20-60 degrees C for 0-25-3 hours, or (S)-alcohols by incubating a racemic alcohol of formula R1-CHOH-R2 in the presence of the enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours.

Query Match 71.08; Score 179; DB 18; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.6e-170;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

39 RHSDVGEKAASVGTPOIQFQHDSDGDKTKLFDATEKAFGVSTLVNNAIVNKS 98
|||||
39 RHSDVGEKAASVGTPOIQFQHDSDGDKTKLFDATEKAFGVSTLVNNAIVNKS 98
|||||
99 VEETTTAEWRKLLAVNLGDVFFGTRGLQRMKNKGLGASIIIMSSIEGFVGDPSLGAYNA 158
|||||
99 VEETTTAEWRKLLAVNLGDVFFGTRGLQRMKNKGLGASIIIMSSIEGFVGDPSLGAYNA 158
|||||
159 SKGAVRIMSKSAALDCALKDYDVVRVTVHPGYIKTPLVDLPGAEAMSORTKTPMGHI 217
|||||
159 SKGAVRIMSKSAALDCALKDYDVVRVTVHPGYIKTPLVDLPGAEAMSORTKTPMGHI 217
|||||

RESULT 2
AAW23409
ID AAW23409 standard; Protein; 251 AA.
AC AAW23409;
DT 27-MAR-1998 (first entry)
XX *Lactobacillus kefir* alcohol dehydrogenase.
DE Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol.
KW *Lactobacillus kefir*.
OS
PH Key Location/Qualifiers
FT Misc-difference 46 /note= "not defined in specification"
FT Misc-difference 47 /note= "not defined in specification"
FT Misc-difference 48 /note= "not defined in specification"
FT Misc-difference 49 /note= "not defined in specification"
FT Misc-difference 50 /note= "not defined in specification"
FT Misc-difference 51 /note= "not defined in specification"
FT Misc-difference 52 /note= "not defined in specification"
FT Misc-difference 53 /note= "not defined in specification"
FT Misc-difference 54 /note= "not defined in specification"
FT Misc-difference 55 /note= "not defined in specification"
FT Misc-difference 56 /note= "not defined in specification"
FT Misc-difference 57 /note= "not defined in specification"

Misc-difference 58 /note= "not defined in specification"
Misc-difference 59 /note= "not defined in specification"
Misc-difference 60 /note= "not defined in specification"
Misc-difference 61 /note= "not defined in specification"
Misc-difference 62 /note= "not defined in specification"
Misc-difference 63 /note= "not defined in specification"
Misc-difference 64 /note= "not defined in specification"
Misc-difference 65 /note= "not defined in specification"
Misc-difference 66 /note= "not defined in specification"
Misc-difference 67 /note= "not defined in specification"
Misc-difference 68 /note= "not defined in specification"
Misc-difference 69 /note= "not defined in specification"
Misc-difference 70 /note= "not defined in specification"
Misc-difference 71 /note= "not defined in specification"
Misc-difference 130 /note= "not defined in specification"
Misc-difference 131 /note= "not defined in specification"
XX EP796914-A2.
XX 24-SEP-1997.
XX 20-MAR-1997; 97EP-0104814.
XX 21-MAR-1996; 96DE-4010984.
XX (BOEF) BOEHRINGER MANNHEIM GMBH.
XX Hummel W, Riebel B;
XX WPI; 1997-459831/43.
XX *Lactobacillus brevis* alcohol dehydrogenase - useful for production of optically active alcohol(s)
XX Example 8; Pages 28-30; 34pp; German.
XX The present *Lactobacillus kefir* alcohol dehydrogenase (ADH) was used in the isolation of a *L. brevis* ADH, which retains at least 95% of its activity after 30 minutes at 20-60 degrees C and can be purified to a specific activity of at least 400 U/mg. The enzyme can be used to produce (R)-alcohols by enantioselective reduction of ketones of formula R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl, aryl or arylenyl (sic) optionally substituted by halogen, NO2, OH or 1-20C alkoxy, "an optionally substituted 1-10C alkylene group, which is substituted by saturated, unsaturated or aromatic heterocycles, or may be an optionally substituted polycondensed saturated and/or aromatic group" (sic) in the presence of the enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours, or (S)-alcohols by incubating a racemic alcohol of formula R1-CHOH-R2 in the presence of the enzyme or cells containing it at 20-60 degrees C for 0.25-3 hours.
XX Sequence 251 AA;
SQ Query Match 18.7%; Score 47; DB 18; Length 251;

Best Local Similarity 100.0%; Pred. No. 1.6e-38;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 153 LGAYNASKGAVRIMSKSAALDCALKDYDVVRNTVHPGYIKTPLVDDL 199
|||||
DB 152 LGAYNASKGAVRIMSKSAALDCALKDYDVVRNTVHPGYIKTPLVDDL 198

RESULT 3
AAV30523
ID AAY30523 standard; peptide; 50 AA.
XX AC AAY30523;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH N-terminal peptide fragment.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound.
XX OS Lactobacillus brevis.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.
XX PR 19-MAR-1998; 98DE-1012004.
XX PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX PI Hummel W, Riebel B;
XX DR WPI; 1999-571842/48.
XX PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
PT recombinant microbial techniques -
XX PS Disclosure; Page 2; 35pp; German.
XX CC This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents the
CC N-terminal fragment of Lactobacillus brevis alcohol dehydrogenase (ADH).

Query Match 14.3%; Score 36; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 37
|||||
DB 1 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 36
RESULT 4
AAV33419
ID AAY33419 standard; peptide; 50 AA.
XX AC AAV33419;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH peptide fragment mutant 2/3.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.

Query Match 14.3%; Score 36; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 37
|||||
DB 1 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 36
RESULT 5
AAV33424
ID AAY33424 standard; peptide; 50 AA.
XX AC AAV33424;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH peptide fragment mutant 2/3.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.

Query Match 14.3%; Score 36; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 37
|||||
DB 1 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 36
RESULT 6
AAV33424
ID AAY33424 standard; peptide; 50 AA.
XX AC AAV33424;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH peptide fragment mutant 2/3.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.

XX DE L. brevis wild-type ADH peptide fragment.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.
XX PR 19-MAR-1998; 98DE-1012004.
XX PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX PI Hummel W, Riebel B;
XX DR WPI; 1999-571842/48.
XX PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
PT recombinant microbial techniques -
XX PS Claim 10; Page 30; 35pp; German.
XX CC This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a wild-type
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX SQ Sequence 50 AA;

Query Match 14.3%; Score 36; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 37
|||||
DB 1 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 36
RESULT 5
AAV33424
ID AAY33424 standard; peptide; 50 AA.
XX AC AAV33424;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH peptide fragment mutant 2/3.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.

Query Match 14.3%; Score 36; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 37
|||||
DB 1 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 36
RESULT 5
AAV33424
ID AAY33424 standard; peptide; 50 AA.
XX AC AAV33424;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH peptide fragment mutant 2/3.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.

Query Match 14.3%; Score 36; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 37
|||||
DB 1 SNRLDGKVAITGGTIGIGLAIATKFEVGEAKVMIT 36
RESULT 5
AAV33424
ID AAY33424 standard; peptide; 50 AA.
XX AC AAV33424;
XX DT 03-DEC-1999 (first entry)
XX DE L. brevis ADH peptide fragment mutant 2/3.
XX KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX OS Lactobacillus brevis.
XX OS Synthetic.
XX PN WO9947684-A2.
XX DT 23-SEP-1999.
XX PF 18-MAR-1999; 99WO-DE00848.

Query Match 10.7%; Score 27; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IITGTLGIGLAIAIKFVEEGAKVMIT 37
DB 10 IITGTLGIGLAIAIKFVEEGAKVMIT 36

RESULT 8
AAV33422
ID AAV33422 standard; peptide; 50 AA.
XX
AC AAV33422;
XX
DT 03-DEC-1999 (first entry)
XX
DE L. brevis ADH peptide fragment mutant 2.
XX
KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX
OS Lactobacillus brevis.
OS Synthetic.
XX
PN WO9947684-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-DE00848.
XX
PR 19-MAR-1998; 98DE-1012004.
XX
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Hummel W, Riebel B;
XX
DR WPI; 1999-571842/48.
XX
PN WO9947684-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-DE00848.
XX
PR 19-MAR-1998; 98DE-1012004.
XX
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Hummel W, Riebel B;
XX
DR WPI; 1999-571842/48.
XX
PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
PT recombinant microbial techniques -
XX
PS Claim 10; Page 30; 35pp; German.
XX
SQ This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX
SQ Sequence 50 AA;

Query Match 10.7%; Score 27; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IITGTLGIGLAIAIKFVEEGAKVMIT 37
DB 10 IITGTLGIGLAIAIKFVEEGAKVMIT 36

RESULT 9
AAV33423
ID AAV33423 standard; peptide; 50 AA.
XX
AC AAV33423;

XX 03-DEC-1999 (first entry)
XX
DE L. brevis ADH peptide fragment mutant 2/2.
XX
KW ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
KW NADPH-dependent dehydrogenase; stereo-selective extraction; racemic;
KW R-hydroxy-compound; keto-compound; S-hydroxy-compound; mutant.
XX
OS Lactobacillus brevis.
OS Synthetic.
XX
PN WO9947684-A2.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-DE00848.
XX
PR 19-MAR-1998; 98DE-1012004.
XX
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Hummel W, Riebel B;
XX
DR WPI; 1999-571842/48.
XX
PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
PT recombinant microbial techniques -
XX
PS Claim 10; Page 30; 35pp; German.
XX
SQ This invention describes a novel method for improving NADH-specificity of
CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
CC in the basicity of the coenzyme-docking region of the enzyme through
CC alteration of the relevant amino acid sequence using genetic technology.
CC The improved dehydrogenase can be used for stereo-selective extraction of
CC R-hydroxy-compounds through enzymatic reduction of the corresponding
CC keto-compound. They can also be used for stereo-selective extraction of
CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
CC pH optimums and improved stability. This sequence represents a mutant
CC Lactobacillus brevis alcohol dehydrogenase (ADH) peptide fragment.
XX
SQ Sequence 50 AA;

Query Match 10.7%; Score 27; DB 20; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 IITGTLGIGLAIAIKFVEEGAKVMIT 37
DB 10 IITGTLGIGLAIAIKFVEEGAKVMIT 36

RESULT 10
AAW23408
ID AAW23408 standard; peptide; 38 AA.
XX
AC AAW23408;
XX
DT 27-MAR-1998 (first entry)
XX
DE Lactobacillus kefir alcohol dehydrogenase amino-terminal.
XX
KW Alcohol dehydrogenase; production; (R)-alcohol; (S)-alcohol;
KW amino-terminal.
XX
OS Lactobacillus kefir.
XX
PN EP796914-A2.
XX
PD 24-SEP-1997.
XX

PP 20-MAR-1997; 97EP-0104814.
 XX 21-MAR-1996; 96DE-4010984.
 PR (BOEF) BOEHRINGER MANNHEIM GMBH.
 PA Hummel W, Riebel B;
 XX WPI; 1997-459831/43.
 PI Lactobacillus brevis alcohol dehydrogenase - useful for production
 XX of optically active alcohol(s)
 PT Example 3; Page 12; 34pp; German.
 PS The present Lactobacillus kefir alcohol dehydrogenase (ADH)
 XX amino-terminal sequence was used in the isolation of a L. brevis
 CC ADH, which retains at least 95% of its activity after 30
 CC minutes at 20-60 degrees C and can be purified to a specific
 CC activity of at least 400 U/mg. The enzyme can be used to produce
 CC (R)-alcohols by enantioselective reduction of ketones of formula
 CC R1-CO-R2, where R1 and R2 = hydrogen (sic) or 1-20C alkyl, alkenyl,
 CC aryl or arylethyl (sic) optionally substituted by halogen, NO2, OH
 CC or 1-20C alkoxy, "an optionally substituted 1-10C alkylene group,
 CC which is substituted by saturated, unsaturated or aromatic
 CC nitrogen, oxygen or sulphur heterocycles, or may be an optionally
 CC substituted polycondensed saturated and/or aromatic group" (sic) in
 CC the presence of the enzyme or cells containing it at 20-60 degrees
 CC C for 0.25-3 hours, or (S)-alcohols by incubating it at 20-60 degrees
 CC of formula R1-CHOH-R2 in the presence of the enzyme or cells
 CC containing it at 20-60 degrees C for 0.25-3 hours.
 XX Sequence 38 AA;
 SQ

Query Match 9.9%; Score 25; DB 18; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 TGGTGLGIGLAIAATKFEVEGAKVMIT 37
 Db 12 TGGTGLGIGLAIAATKFEVEGAKVMIT 36
 RESULT 11
 AAY33413
 ID AAY33413 standard; Protein; 34 AA.
 XX
 AC AAY33413;
 XX
 DT 03-DEC-1999 (first entry)
 DE L. brevis NADP-dependent oxidoreductase peptide fragment 1.
 XX
 DE ADH; alcohol dehydrogenase; NADH-specificity; coenzyme docking region;
 KW NADPH-dependent dehydrogenase; stereo-selective docking region;
 KW R-hydroxy-compound; keto-compound; S-hydroxy-compound.
 XX
 OS Lactobacillus brevis.
 XX
 XX WO9947684-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-DE00848.
 XX
 PR 19-MAR-1998; 98DE-1012004.
 XX
 PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
 XX
 PI Hummel W, Riebel B;
 XX
 DR WPI; 1999-571842/48.
 XX

PT Improving NADH-specificity of NADPH-dependent dehydrogenases by
 XX recombinant microbial techniques -
 PS Example 4; Page 27; 35pp; German.
 XX
 CC This invention describes a novel method for improving NADH-specificity of
 CC preferred NADPH-dependent dehydrogenase. The method comprises a reduction
 CC in the basicity of the coenzyme-docking region of the enzyme through
 CC alteration of the relevant amino acid sequence using genetic technology.
 CC The improved dehydrogenase can be used for stereo-selective extraction of
 CC R-hydroxy-compounds through enzymatic reduction of the corresponding
 CC keto-compound. They can also be used for stereo-selective extraction of
 CC S-hydroxy-compounds from racemic mixtures, through enzymatic oxidation of
 CC the R-hydroxy-compound. The dehydrogenases have improved temperature and
 CC pH optimums and improved stability. This sequence represents a
 CC Lactobacillus brevis alcohol dehydrogenase (ADH) coenzyme binding site
 CC described in the method of the invention.
 XX Sequence 34 AA;
 SQ

Query Match 7.9%; Score 20; DB 20; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.2e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 GIGLAIAATKFEVEGAKVMIT 37
 Db 1 GIGLAIAATKFEVEGAKVMIT 20
 RESULT 12
 ABG07478
 ID ABG07478 standard; Protein; 120 AA.
 XX
 AC ABG07478;
 XX
 DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #7459.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS71665.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 37837; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques

to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 3.2%; Score 8; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 TLVNNAGI 93
Db 82 TLVNNAGI 89
|||||

RESULT 13
ABB40547
ID ABB40547 standard; Peptide; 120 AA.

AC ABB40547;

DT 04-FEB-2002 (first entry)

DE Peptide #8053 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483447/52.

PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human foetal liver -

PS Claim 27; SEQ ID NO 33182; 639pp + sequence listing; English.

The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human foetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 120 AA;

Query Match 3.2%; Score 8; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
Db 87 LVNNAGIA 94
|||||

RESULT 14
AAM74176

ID AAM74176 standard; Protein; 120 AA.

AC AAM74176;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34482.

KW Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -

PS Example 4; SEQ ID NO: 34482; 658pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.

SQ Sequence 120 AA;

Query Match 3.2%; Score 8; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
Db 87 LVNNAGIA 94
|||||

RESULT 15

Job time : 34 secs

AAU5352
ID AAU5352 standard; Protein; 136 AA.
AC AAU5352;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #16248.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PE 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59569.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID No 16547; 1069pp; English.
XX
CC Sequences AAU39105-AAU69017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 136 AA;
Query Match 3.2%; Score 8; DB 22; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 88 VNNAGIAY 95
| | | | | | | | | |
DB 34 VNNAGIAY 41

Search completed: October 30, 2002, 15:48:00

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:46:30 ; Search time 19 Seconds
(without alignments)
1274.448 Million cell updates/sec

Title: US-09-910-033A-2
Perfect score: 252
Sequence: 1 MSNRDQKVAITGTLGIG.....NESKFATGSEFVDGGYTAQ 252

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	4.0	29	S14099	12-alpha-hydroxyst
2	10	4.0	260	B87668	2-deoxy-D-gluconat
3	9	3.6	250	T20258	hypothetical prote
4	9	3.6	267	T11579	probable short cha
5	9	3.6	283	E87603	hypothetical prote
6	9	3.6	289	D69825	glucose 1-dehydrog
7	9	3.6	303	T46064	short-chain alcoh
8	8	3.2	238	G83126	probable short-cha
9	8	3.2	249	S47055	hypothetical prote
10	8	3.2	251	T4180	hypothetical prote
11	8	3.2	251	T06364	probable short-cha
12	8	3.2	251	AC0103	2-deoxy-D-gluconat
13	8	3.2	252	D83766	3-oxoacyl-(acyl-ca
14	8	3.2	252	G72618	hypothetical prote
15	8	3.2	254	B87630	hypothetical prote
16	8	3.2	254	AD3182	short chain dehydr
17	8	3.2	257	C98348	reductase (AL13282
18	8	3.2	257	AD2934	short chain dehydr
19	8	3.2	263	A98301	probable short-cha
20	8	3.2	263	AG2982	dehydrogenase Atu3
21	8	3.2	272	T47354	alcohol dehydrogen
22	8	3.2	276	JC5285	carboxyl reductase
23	8	3.2	277	1 RDHUCB	carboxyl reductase
24	8	3.2	277	JC5284	carboxyl reductase
25	8	3.2	277	T29800	hypothetical prote
26	8	3.2	307	S62472	probable Methylthi
27	8	3.2	335	T24540	hypothetical prote
28	8	3.2	336	A47542	short-chain alcoh
29	8	3.2	475	T00620	probable amino aci

amino acid transpo
oxidoreductase hom
ntpQ protein - Ent
hemoglobin alpha-2
hemoglobin alpha-1
hemoglobin alpha-I
hemoglobin alpha c
hemoglobin alpha c
3-octaprenyl-4-hyd
ribosomal protein
ribosomal protein
hypothetical prote
3-hydroxybutyrate
shikimate kinase I
hypothetical prote
pyrrolidone carbox

ALIGNMENTS

RESULT 1

S14099
12-alpha-hydroxysteroid dehydrogenase - Clostridium sp. (strain C 48-50)
C:Species: Clostridium sp.
A:Variety: strain C 48-50
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S14099
R: Braun, M.; Luensdorf, H.; Bueckmann, A.F.
Eur. J. Biochem. 196, 439-450, 1991
A:Title: 12-alpha-hydroxysteroid dehydrogenase from Clostridium group P, strain C 48-50
A:Reference number: S14099; MUID:91177018
A:Accession: S14099
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-29 <BRA>

Query Match 4.0%; Score 10; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DGKVAITGG 15
|||||

DB 4 DGKVAITGG 13
|||||

RESULT 2

B87668
2-deoxy-D-gluconate 3-dehydrogenase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: B87668
R: Nierman, W.C.; DeBlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kc n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: B87668
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <STO>
A:Cross-references: GB:AE005673; NID:gl3425088; PIDN:AAK25342.1; GSPDB:GN00148
C:Genetics: CC380

Query Match 4.0%; Score 10; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 LAVNLGVEFF 120
|||||

Db 116 LAVNLGVFF 125

RESULT 3

T20258 hypothetical protein C55A6.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C:Accession: T20258

R:Kershaw, J.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19243

A:Accession: T20258

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-250 <N1>

A:Cross-references: EMBL:Z81051; PIDN:CAB02866.1; GSPDB:GN00023; CBSP:C55A6.6

A:Experimental source: clone C55A6

C:Genetics:

A:Gene: CBSP:C55A6.6

A:Map position: 5

A:Introns: 43/3; 99/3; 217/3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.6%; Score 9; DB 2; Length 250;

Best Local Similarity 100.0%; Pred. No. 0.39;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNAGIATV 95

Db 85 LVNAGIATV 93

|||||

RESULT 4

T11579

probable short chain alcohol dehydrogenase CPRD12, drought-inducible - cowpea

C:Species: Vigna unguiculata (cowpea)

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000

C:Accession: T11579

R:Tuchi, S.; Yamaguchi-Shinozaki, K.; Urao, T.; Shinozaki, K.

J. Plant Res. 109, 415-424, 1996

A:Title: Characterization of two cDNAs for novel drought-inducible genes in the highly

A:Reference number: Z17293

A:Accession: T11579

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-267 <IUC>

A:Cross-references: EMBL:D88121

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.6%; Score 9; DB 2; Length 267;

Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAITGG 15

Db 16 GKVAITGG 24

|||||

RESULT 5

E87603

hypothetical protein CC2861 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 03-Aug-2001

C:Accession: E87603

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.W.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: AB87249; MUID:21173698; PMID:11259647

A:Accession: E87603

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-283 <STO>

A:Cross-references: GB:AE005673; NID:gl3424475; PIDN:AAK24825.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2861

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.6%; Score 9; DB 2; Length 283;

Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNAGIATV 95

Db 84 LVNAGIATV 92

|||||

RESULT 6

D69825

glucose 1-dehydrogenase homolog yhfF - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: D69825

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; B

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; G

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo,

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lard

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; M

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scat

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchi

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshic

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil

A:Reference number: A69580; MUID:98044033

A:Accession: D69825

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-289 <KUN>

A:Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12784.1; PID:g2633

A:Experimental source: strain 168

C:Genetics:

A:Gene: yhfF

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F:46-225/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 3.6%; Score 9; DB 2; Length 289;

Best Local Similarity 100.0%; Pred. No. 0.45;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAITGG 15

Db 45 GKVAITGG 53

|||||

RESULT 7

T46064

short-chain alcohol dehydrogenase-like protein - Arabidopsis thaliana

N:Alternate names: protein T18N14.60

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46064

R:Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke,

submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23013

A:Accession: T46064

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-303

A:Cross-references: EMBL:AL132968

A:Experimental source: cultivar Columbia; BAC clone T18N14

C:Genetics:

A:Map position: 3

A:Introns: 31/2

A:Note: T18N14.60

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.6%; Score 9; DB 2; Length 303;

Best Local Similarity 100.0%; Pred. No. 0.46;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GKVAITGG 15

Db 34 GKVAITGG 42

RESULT 8

G83126

probable short-chain dehydrogenase PA4162 [imported] - Pseudomonas aeruginosa (strain PA

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G83126

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: AB2950; MUID:20437337

A:Accession: G83126

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-238 <STO>

A:Cross-references: GB:AE004832; GB:AE004091; NID:g9950360; PIDN:AAG07549.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA4162

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2%; Score 8; DB 2; Length 238;

Best Local Similarity 100.0%; Pred. No. 4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LVNNAGIA 94

Db 73 LVNNAGIA 80

RESULT 9

S47055

hypothetical protein 5 - Xanthobacter sp.

C:Species: Xanthobacter sp.

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999

C:Accession: S47055

R:Swaving, J.; Weijers, C.A.G.M.; van Ooyen, A.J.J.; de Bont, J.A.M.

submitted to the EMBL Data Library, June 1994

A:Description: Plasmid of Xanthobacter Py2 mutants in epoxycane degradation; exp

A:Reference number: S47051

A:Accession: S47055

A:Molecule type: DNA

A:Residues: 1-249 <SWA>

A:Cross-references: EMBL:X79863; NID:g520947; PIDN:CAA56245.1; PID:g520952

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F:5-181/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 3.2%; Score 8; DB 2; Length 249;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LVNNAGIA 94

Db 82 LVNNAGIA 89

RESULT 10

T24180

hypothetical protein R11D1.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T24180

R:Steward, C.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19850

A:Accession: T24180

A>Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: DNA

A:Residues: 1-251 <WIL>

A:Cross-references: EMBL:Z75547; PIDN:CAA99897.1; GSPDB:GN00023; CESP:R11D1.11

A:Experimental source: clone R11D1

C:Genetics:

A:Gene: CESP:R11D1.11

A:Map position: 5

A:Introns: 56/3; 157/1; 196/3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2%; Score 8; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 LVNNAGIA 94

Db 87 LVNNAGIA 94

RESULT 11

T06364

probable short-chain alcohol dehydrogenase (EC 1.1.1.1-) - tomato (fragment)

C:Species: Lycopersicon esculentum (tomato)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000

C:Accession: T06364

R:Jacobsen, S.E.; Olszewski, N.E.

Planta 198, 78-86, 1996

A:Title: Gibberellins regulate the abundance of RNAs with sequence similarity to prot

A:Reference number: Z15627; MUID:96158488

A:Accession: T06364

A>Status: preliminary; translated from GB/EMBL/DBBJ

A:Molecule type: mRNA

A:Residues: 1-251 <JAC>

A:Cross-references: EMBL:U21801; NID:g717141; PIDN:AAB00109.1; PID:g717142

A:Experimental source: cultivar Moneymaker

C:Genetics:

A:Gene: GAD3

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: alcohol metabolism; oxidoreductase

Query Match 3.2%; Score 8; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GKVAITGG 14

Db 2 GKVAITGG 9

RESULT 12

AC0103

2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125) [imported] - Yersinia pestis (stra

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C:Accession: AC0103

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, N

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AC0103

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-251 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89686.1; PID:g15978913; GSPDB:GN00175

C:Genetics:

A:Gene: kduD2

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: oxidoreductase

Query Match 3.2% Score 8; DB 2; Length 251;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GKVAITG 14

|||||||

Db 8 GKVAITG 15

RESULT 13

D83766

3-oxoacyl-(acyl-carrier protein) reductase BH0932 [imported] - Bacillus halodurans (strain C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: D83766

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Reference number: A83650; MUID:20512582; PMID:11058132

C:Accession: D83766

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-252 <STO>

A:Cross-references: GB:AP001510; GB:BA000004; MID:g10173440; PIDN:BA04651.1; GSPDB:GN00

C:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0932

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2% Score 8; DB 2; Length 252;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27 FVEEGAKV 34

|||||||

Db 27 FVEEGAKV 34

RESULT 14

G72618

hypothetical protein APE1408 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: G72618

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-do, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; MUID:99310339

C:Accession: G72618

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-252 <KAW>

A:Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80405.1; PID:g5105091

C:Experimental source: strain K1

C:Genetics:

A:Gene: APE1408

C:Superfamily: Aeropyrum pernix hypothetical protein APE1408

Query Match 3.2% Score 8; DB 2; Length 252;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 IEGFVGDP 151

Db 225 IEGFVGDP 232

RESULT 15

B87630

hypothetical protein CC3076 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: B87630

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

C:Accession: B87630

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-254 <STO>

A:Cross-references: GB:AE005673; NID:g13424728; PIDN:AAK25038.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3076

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.2% Score 8; DB 2; Length 254;

Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GKVAITG 14

|||||||

Db 8 GKVAITG 15

Search completed: October 30, 2002, 15:48:59

Job time : 20 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:40 ; Search time 12 seconds

(without alignments)
813.111 Million cell updates/sec

Title: US-09-910-033a-2

Perfect score: 252

Sequence: 1 MSNRLDGKVAITGTLGIG.....NESKFGTSEFVVDGGYTAQ 252

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	4.0	29	12AH_CLOS4	P21215 clostridium
2	9	3.6	289	YHDF_BACSU	O07575 bacillus su
3	8	3.2	251	CHBR2_CAEEL	Q21929 caenorhabdi
4	8	3.2	276	1 DHCA_HUMAN	P16152 homo sapien
5	8	3.2	276	1 DHCA_HUMAN	P47727 rattus norv
6	8	3.2	307	1 YAC2_SCHPO	O09816 schizosacch
7	8	3.2	336	1 TS2_MAIZE	P50160 zea mays (m
8	7	2.8	103	1 NTPG_ENTHR	P43455 enterococu
9	7	2.8	141	1 HBA_MUSPF	P20243 mustela put
10	7	2.8	141	1 HBA_SPECI	P09420 spermophili
11	7	2.8	141	1 HBA_SPEPA	P11750 spermophili
12	7	2.8	178	1 BDH_BOVIN	O02337 bos taurus
13	7	2.8	205	1 VATO_HUMAN	Q99437 homo sapien
14	7	2.8	211	1 PCPI_SULSO	P58201 sulfolobus
15	7	2.8	228	1 FLPA_METVO	P35553 methanococ
16	7	2.8	241	1 BUDC_KLETE	Q04520 klebsiella
17	7	2.8	241	1 PHBB_RHIME	P50205 rhizobium m
18	7	2.8	241	1 PHBB_ZOORA	P23238 zoogloea ra
19	7	2.8	242	1 PHBG_HAEIN	P43713 haemophilus
20	7	2.8	242	1 MYF6_CHICK	Q01795 gallus gall
21	7	2.8	242	1 PHAB_PARDE	P50204 paracoccus
22	7	2.8	244	1 PHAB_ECOLI	P25716 escherichia
23	7	2.8	244	1 PHBG_SALTY	O85141 salmonella
24	7	2.8	244	1 PHBG_VIBCH	Q9kqh7 vibrio chol
25	7	2.8	244	1 PHBG_VIBHA	P55336 vibrio harv
26	7	2.8	245	1 NODG_RHIME	P76234 rhizobium m
27	7	2.8	245	1 NODG_RHIS3	P62332 rhizobium s
28	7	2.8	246	1 PHBG_BACSU	P51831 bacillus su
29	7	2.8	246	1 PHBG_THEMEA	O9x248 thermotoga
30	7	2.8	246	1 NODG_AZOR	P17611 azospirillum
31	7	2.8	247	1 PHBG_MYCTU	Q48930 mycobacteri
32	7	2.8	247	1 FAGI_SYNY3	P73574 synechocyst
33	7	2.8	247	1 YGFF_ECOLI	P52037 escherichia

34	7	2.8	248	1	FABG_AQUAE	O67610 aquifex ae
35	7	2.8	248	1	FABG_CHLPN	O928p2 chlamydia p
36	7	2.8	248	1	PHAB_ACISP	P50203 acinetobact
37	7	2.8	250	1	LINX_PSEPA	P50198 pseudomonas
38	7	2.8	251	1	Y325_THEMEA	O9w790 thermotoga
39	7	2.8	252	1	DLTE_BACSU	P39577 bacillus su
40	7	2.8	253	1	3BHD_COMTE	P19871 comamonas t
41	7	2.8	253	1	KDUD_ERWCH	O05528 erwinia chr
42	7	2.8	254	1	IDNO_ECOLI	P39345 escherichia
43	7	2.8	254	1	KDUD_BACSU	P50842 bacillus su
44	7	2.8	255	1	2BHD_STREX	P19992 streptomyce
45	7	2.8	255	1	FABG_MYCAV	O07399 mycobacteri

ALIGNMENTS

RESULT 1
12AH_CLOS4
ID 12AH_CLOS4 STANDARD; PRT; 29 AA.
AC P21215;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE 12-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.176) (Fragment).
OS Clostridium sp. (strain C 48-50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1507;
RN [1]
RP SEQUENCE.
RX MEDLINE=91177018; PubMed=2007406;
RA Braun M., Luensdorf H., Bueckmann A.F.;
RT "12 alpha-hydroxysteroid dehydrogenase from Clostridium group P,
strain C 48-50. Production, purification and characterization.";
RL Eur. J. Biochem. 196:439-450(1991).
CC -!- FUNCTION: CATALYSES THE OXIDATION OF THE 12-ALPHA-HYDROXYL GROUP
OF BILE ACIDS, BOTH IN THEIR FREE AND CONJUGATED FORM. ALSO ACTS
ON BILE ALCOHOLS.
CC -!- CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-
cholananate + NADP(+) = 3-alpha,7-alpha-dihydroxy-12-oxo-5-beta-
cholananate + NADPH.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- MISCELLANEOUS: THE THERMOSTABILITY OF THE ENZYME IS GREATLY
INCREASED DUE TO NADP BINDING.
DR PIR; SI4099; SI4099.
KW Oxidoreductase; NADP.
FT NON_TER 29
SQ SEQUENCE 29 AA; 2900 MW; A827DB34DB6C8812 CRC64;

Query Match 4.0%; Score 10; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 DGKVAITGG 15
|||||||
DB 4 DGKVAITGG 13

RESULT 2
YHDF_BACSU
ID YHDF_BACSU STANDARD; PRT; 289 AA.
AC O07575;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical oxidoreductase yhdF (EC 1.-.-.-).
GN YHDF.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; Y14082; CAA74490.1;
CC EMBL; 299109; CAB12784.1;
CC HSSP; P50162; IAE1.
CC Subtilist; BG13012; yHdF.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PROSITE; PS00061; ADH_SHORT; 1.
CC KW Hypothetical protein; Oxidoreductase; Complete proteome.
CC FT NP_BIND 49 73 NAD OR NADP (BY SIMILARITY).
CC FT ACT_SITE 194 194 BY SIMILARITY.
CC SQ SEQUENCE 289 AA; 31509 MW; 4EC98C62B9241BC1 CRC64;

Query Match 3.6%; Score 9; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GKVAITGG 15
DB 45 GKVAITGG 53

RESULT 3
CBER2_CAEEL STANDARD; PRT; 251 AA.
AC Q21929;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Probable carbonyl reductase [NADPH] (EC 1.1.1.184) (NADPH-dependent
DE carbonyl reductase).
GN R1D1.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Steward C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) -> R-CO-R' + NADPH (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; 275547; CAA99897.1;
CC HSSP; P08074; LCYD.
CC WormPep; R1D1.11; CE06316.
CC InterPro; IPR002198; ADH_short.
CC -----

DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Mitochondrion.
FT NP_BIND 11 41 NADP (ADP RIBOSE PART) (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
FT DOMAIN 203 206 POLY-LYS.
SQ SEQUENCE 251 AA; 27188 MW; 4F51C9FA802D797D CRC64;

Query Match 3.2%; Score 8; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
DB 87 LVNNAGIA 94

RESULT 4
DHCA_HUMAN STANDARD; PRT; 276 AA.
AC P16152;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl
DE reductase 1) (Prostaglandin-E2 9-reductase) (EC 1.1.1.189)
DE (Prostaglandin 9-ketoreductase) (15-hydroxyprostaglandin dehydrogenase
DE [NADP+]) (EC 1.1.1.197).
GN CBRI OR CBR OR CRN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=89034082; PubMed=3141401;
RA Wermuth B., Bohren K.M., Heinemann G., von Wartburg J.-P.,
RA Gabbay K.H.;
RT "Human carbonyl reductase. Nucleotide sequence analysis of a cDNA and
RT amino acid sequence of the encoded protein.";
RL J. Biol. Chem. 263:16185-16188(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Breast;
RX MEDLINE=90212644; PubMed=2182121;
RA Forrest G.L., Akman S., Krutzik S., Paxton R.J., Sparkes R.S.,
RA Doroshov J., Felsted R.L., Mohandas T., Bachur N.R.;
RT "Induction of a human carbonyl reductase gene located on chromosome
RT 21.";
RL Biochim. Biophys. Acta 1048:149-155(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92017676; PubMed=1921984;
RA Forrest G.L., Akman S., Doroshov J., Rivera H., Kaplan W.D.;
RT "Genomic sequence and expression of a cloned human carbonyl reductase
RT gene with daunorubicin reductase activity.";
RL Mol. Pharmacol. 40:502-507(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98414514; PubMed=9740676;
RA Watanabe K., Sugawara C., Ono A., Fukuzumi Y., Itakura S.,
RA Yamazaki M., Tashiro H., Osoegawa K., Soeda E., Nomura T.;
RT "Mapping of a novel human carbonyl reductase, CBR3, and ribosomal
RT pseudogenes to human chromosome 21q22.2.";
RL Genomics 52:95-100(1998).
RN [5]
RP SEQUENCE FROM N.A.
RA Shibuya K., Kudoh J., Minoshima S., Kawasaki K., Nakatoh E.,
RA Shintani A., Asakawa S., Shimizu N.;
RT "Genomic sequencing of 1.2-Mb region on human chromosome 21q22.2.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

[6]
SEQUENCE FROM N.A.
MEDLINE=20289793; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Okhi M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald A., Rump A., Shilubaya K., Kawasaki K., Asakawa S.,
RA Rosenthal A., Kudoh J., Shibuya K., Nagamine K., Antonarakis S.E.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Brandt P.,
RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riessmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Mizetic D., Francis F.,
RA Leinhardt H., Reinhardt R., Yaspo M.-L.;
RA "The DNA sequence of human chromosome 21.";
RA Nature 405:311-319(2000).
[7]
PARTIAL SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.
MEDLINE=93133816; PubMed=8421682;
RA Krook M., Ghosh D., Stromberg R., Carlquist M., Joernvall H.;
RA "Carboxyethyllysine in a protein: native carbonyl reductase/NADP(+)-
RA dependent prostaglandin dehydrogenase.";
RA Proc. Natl. Acad. Sci. U.S.A. 90:502-506(1993).
CC -1- FUNCTION: CATALYZE THE REDUCTION OF A WIDE VARIETY OF CARBONYL
CC COMPOUNDS INCLUDING THE ANTITUMOR ANTHRACYCLINE ANTIBIOTICS.
CC CAN CONVERT PROSTAGLANDIN E2 TO PROSTAGLANDIN F2-ALPHA.
CC -1- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.
CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9,11,15-trihydroxyprosta-5,13-
CC dienate + NADP(+) = (5Z,13E)-(15S)-11,15-dihydroxy-9-oxoprosta-
CC 5,13-dienate + NADPH.
CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-11-alpha,15-dihydroxy-9-
CC oxoprosta-13-enate + NADP(+) = (5Z,13E)-11-alpha-hydroxy-9,15-
CC dihydroprosta-13-enate + NADPH.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.

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DR EMBL; J04056; AAA52070.1; -;
DR EMBL; M62420; AAA17881.1; -;
DR EMBL; AB003351; BAA33498.1; -;
DR EMBL; AP000688; BAA89424.1; -;
DR EMBL; AP001724; BAA95508.1; -;
DR PIR; A31912; RDHUCB.
DR PIR; S09013; S09013.
DR HSP; P14061; 1FDW.
DR MIM; 114830; -;
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00081; GDRDH.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR Oxidoreductase; NADP; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT NP_BIND 9 33 NADP (BY SIMILARITY).
FT ACT_SITE 193 193 BY SIMILARITY.
SQ SEQUENCE 276 AA; 30244 MW; 78E3065F5677733 CRC64;
Query Match 3.2%; Score 8; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 LVNNAGIA 94

Db 86 LVNNAGIA 93
|||||||
RESULT 5
DHCA_RAT STANDARD; PRT; 276 AA.
AC P47727;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl
DE reductase 1).
GN CBRI OR CBR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
RX MEDLINE=95220378; PubMed=7705364;
RA Wermuth B., Maeder-Heinemann G., Ernst E.;
RA "Cloning and expression of carbonyl reductase from rat testis.";
RA Eur. J. Biochem. 228:473-479(1995).
CC -1- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.

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DR EMBL; X84349; CAA59088.1; -;
DR EMBL; X95986; CAA65230.1; -;
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00081; GDRDH.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR Oxidoreductase; NADP; Acetylation.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT NP_BIND 9 33 NADP (BY SIMILARITY).
FT ACT_SITE 193 193 BY SIMILARITY.
SQ SEQUENCE 276 AA; 30447 MW; 99B9E77C5E9222AB CRC64;
Query Match 3.2%; Score 8; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 LVNNAGIA 94
|||||||
Db 86 LVNNAGIA 93
RESULT 6
YAC2_SCHPO STANDARD; PRT; 307 AA.
AC Q09816;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 33.9 kDa protein C16C9.02C in chromosome 1.
GN SPAC16C9.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN (1)
RP SEQUENCE FROM N.A.

RC STRAIN=972;
RA Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (Oct-1995) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE PNP/MTAP FAMILY 2 OF PHOSPHORYLASES.
CC
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DR EMBL: Z54366; CAA91190.1; -;
DR HSP: Q13126; ICB0.
DR InterPro: IPR001369; Mtap_PNP.
DR Pfam: PF00896; Mtap_PNP; 1.
DR PROSITE: PS01240; PNP_MTPAP.2; 1.
KW Hypothetical protein; Transferase; Glycosyltransferase.
SQ SEQUENCE 307 AA; 33847 MW; A289285BFD438067 CRC64;

Query Match 3.2%; Score 8; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 135 GASTIIMS 142
DB 192 GASTIIMS 199
|||||

RESULT 7
TS2_MAIZE
ID TS2_MAIZE STANDARD; PRT; 336 AA.
AC P50160;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Sex determination protein tasselseed 2.
GN TS2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. W22;
RC MEDLINE=93364991; PubMed=8358795;
RA Delong A., Calderon-Urrea A., Dellaporta S.L.;
RT Sex determination gene TASSELSEED2 of maize encodes a short-chain
RT alcohol dehydrogenase required for stage-specific floral organ
RT abortion.;
RL Cell 74:757-768(1993).
CC -1- FUNCTION: REQUIRED FOR STAGE-SPECIFIC FLORAL ORGAN ABORTION.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----

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CC -----

DR EMBL: L20621; AAC37345.1; -;
DR HSP: P19992; IHDC.
DR MaizeDB: 56963; -;
DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase; Developmental protein.
FT NP_BIND 59 83
FT ACT_SITE 207 207
SQ SEQUENCE 336 AA; 35204 MW; 4E273D6152B0BB99 CRC64;

Query Match 3.2%; Score 8; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 RLDGKVAI 11
DB 52 RLDGKVAI 59
|||||

RESULT 8
NTPG_ENTHR
ID NTPG_ENTHR STANDARD; PRT; 103 AA.
AC P43455;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE V-type sodium ATP synthase subunit G (EC 3.6.3.14) (Na(+)-
DE translocating ATPase subunit G).
GN NTPG OR NTPQ.
OS Enterococcus hirae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1354;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 9790;
RA Takase K., Kakinuma S., Yamato I., Konishi K., Igarashi K.,
RA Kakinuma Y.;
RT "Sequencing and characterization of the ntp gene cluster for
RT vacuolar-type Na(+)-translocating ATPase of Enterococcus hirae.";
RL J. Biol. Chem. 269:11037-11044(1994).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 9790;
RC MEDLINE=94193617; PubMed=8144530;
RA Solioz M., Davies K.;
RT Operon of vacuolar-type Na(+)-ATPase of Enterococcus hirae.";
RL J. Biol. Chem. 269:9453-9459(1994).
CC -1- FUNCTION: INVOLVED IN ATP-DRIVEN SODIUM EXTRUSION.
CC -1- SIMILARITY: BELONGS TO THE V-ATPASE F SUBUNIT FAMILY.
CC -----

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DR EMBL: D17462; BAA04274.1; -;
DR EMBL: X76913; CAA54240.1; -;
DR InterPro: IPR002841; ATP-synt_F.
DR Pfam: PF01990; ATP-synt_F; 1.
DR Propom; PD003811; ATP-synt_F; 1.
KW Hydrolyase; ATP synthetase; Hydrogen ion transport.
SQ SEQUENCE 103 AA; 11410 MW; 5F452721633D3960 CRC64;

Query Match 2.8%; Score 7; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15 GTLIGL 21
DB 81 GTLIGL 87
|||||

RESULT 9
NTPG_ENTHR
ID NTPG_ENTHR STANDARD; PRT; 103 AA.
AC P43455;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE V-type sodium ATP synthase subunit G (EC 3.6.3.14) (Na(+)-
DE translocating ATPase subunit G).
GN NTPG OR NTPQ.
OS Enterococcus hirae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1354;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 9790;
RC MEDLINE=94193617; PubMed=8144530;
RA Solioz M., Davies K.;
RT Operon of vacuolar-type Na(+)-ATPase of Enterococcus hirae.";
RL J. Biol. Chem. 269:9453-9459(1994).
CC -1- FUNCTION: INVOLVED IN ATP-DRIVEN SODIUM EXTRUSION.
CC -1- SIMILARITY: BELONGS TO THE V-ATPASE F SUBUNIT FAMILY.
CC -----

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DR EMBL: D17462; BAA04274.1; -;
DR EMBL: X76913; CAA54240.1; -;
DR InterPro: IPR002841; ATP-synt_F.
DR Pfam: PF01990; ATP-synt_F; 1.
DR Propom; PD003811; ATP-synt_F; 1.
KW Hydrolyase; ATP synthetase; Hydrogen ion transport.
SQ SEQUENCE 103 AA; 11410 MW; 5F452721633D3960 CRC64;

PRINTS; PR00612; ALPHAHAE. DR PROSITE; PS01033; GLOBIN; 1. KW Heme; Oxygen transport; Transp; Erythrocyte. FT METAL 58 58 IRON (HEME DISTAL LIGAND). FT METAL 87 87 IRON (HEME PROXIMAL LIGAND). SQ SEQUENCE 141 AA; 15192 MW; 365EA7E98227347B CRC64;

Query Match 2.8%; Score 7; DB 1; Length 141; Best Local Similarity 100.0%; Pred. No. 11; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 VDDLPGA 202 Db 73 VDDLPGA 79

RESULT 11 HBA_SPEA ID HBA_SPEA STANDARD; PRT; 141 AA. DT 01-OCT-1989 (Rel. 12, Created) DT 01-NOV-1990 (Rel. 16, Last sequence update) DT 01-JUN-1994 (Rel. 29, Last annotation update) DE Hemoglobin alpha chain. OS Spermophilus parryi (Arctic ground squirrel) (Citellus parryi). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae; OC Spermophilus OC NCBI_TaxID=9999; RN [1] RP SEQUENCE. RX MEDLINE=87274834; PubMed=3608432; Duffy L.K., Ehrhardt M.M., Genaux C.T., Florant G.L.; "The primary structure of the hemoglobin alpha-chain of the arctic ground squirrel."; Comp. Biochem. Physiol. 87B:189-193(1987). DR PIR; JU0165; JU0165. DR HSSP; P01922; 1B20. DR InterPro; IPR002338; Alpha.haem. DR InterPro; IPR000971; Globin. DR Pfam; PF00042; globin; 1. DR PRINTS; PR00612; ALPHAHAE. DR PROSITE; PS01033; GLOBIN; 1. KW Heme; Oxygen transport; Transp; Erythrocyte. FT METAL 58 58 IRON (HEME DISTAL LIGAND). FT METAL 87 87 IRON (HEME PROXIMAL LIGAND). SQ SEQUENCE 141 AA; 15047 MW; FF0D9DF6552D1F72 CRC64;

Query Match 2.8%; Score 7; DB 1; Length 141; Best Local Similarity 100.0%; Pred. No. 11; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 VDDLPGA 202 Db 73 VDDLPGA 79

RESULT 12 BDH_BOVIN ID BDH_BOVIN STANDARD; PRT; 178 AA. DT 01-OCT-1993 (Rel. 27, Created) DT 01-OCT-1993 (Rel. 27, Last sequence update) DT 01-OCT-1996 (Rel. 34, Last annotation update) DE D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) (BDH) (3-hydroxybutyrate dehydrogenase) (Fragments). GN BDH. OS Bos taurus (Bovine). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. OC NCBI_TaxID=9913; RN [1]

PRINTS; PR00612; ALPHAHAE. DR PROSITE; PS01033; GLOBIN; 1. KW Heme; Oxygen transport; Transp; Erythrocyte. FT METAL 58 58 IRON (HEME DISTAL LIGAND). FT METAL 87 87 IRON (HEME PROXIMAL LIGAND). SQ SEQUENCE 141 AA; 15192 MW; 365EA7E98227347B CRC64;

Query Match 2.8%; Score 7; DB 1; Length 141; Best Local Similarity 100.0%; Pred. No. 11; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 VDDLPGA 202 Db 73 VDDLPGA 79

RESULT 11 HBA_SPEA ID HBA_SPEA STANDARD; PRT; 141 AA. DT 01-OCT-1989 (Rel. 12, Created) DT 01-NOV-1990 (Rel. 16, Last sequence update) DT 01-JUN-1994 (Rel. 29, Last annotation update) DE Hemoglobin alpha chain. OS Spermophilus parryi (Arctic ground squirrel) (Citellus parryi). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae; OC Spermophilus OC NCBI_TaxID=9999; RN [1] RP SEQUENCE. RX MEDLINE=87274834; PubMed=3608432; Duffy L.K., Ehrhardt M.M., Genaux C.T., Florant G.L.; "The primary structure of the hemoglobin alpha-chain of the arctic ground squirrel."; Comp. Biochem. Physiol. 87B:189-193(1987). DR PIR; JU0165; JU0165. DR HSSP; P01922; 1B20. DR InterPro; IPR002338; Alpha.haem. DR InterPro; IPR000971; Globin. DR Pfam; PF00042; globin; 1. DR PRINTS; PR00612; ALPHAHAE. DR PROSITE; PS01033; GLOBIN; 1. KW Heme; Oxygen transport; Transp; Erythrocyte. FT METAL 58 58 IRON (HEME DISTAL LIGAND). FT METAL 87 87 IRON (HEME PROXIMAL LIGAND). SQ SEQUENCE 141 AA; 15199 MW; D0EA19424B09A88E CRC64;

Query Match 2.8%; Score 7; DB 1; Length 141; Best Local Similarity 100.0%; Pred. No. 11; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 VDDLPGA 202 Db 73 VDDLPGA 79

RESULT 12 BDH_BOVIN ID BDH_BOVIN STANDARD; PRT; 178 AA. DT 01-OCT-1993 (Rel. 27, Created) DT 01-OCT-1993 (Rel. 27, Last sequence update) DT 01-OCT-1996 (Rel. 34, Last annotation update) DE D-beta-hydroxybutyrate dehydrogenase (EC 1.1.1.30) (BDH) (3-hydroxybutyrate dehydrogenase) (Fragments). GN BDH. OS Bos taurus (Bovine). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. OC NCBI_TaxID=9913; RN [1]

PRINTS; PR00612; ALPHAHAE. DR PROSITE; PS01033; GLOBIN; 1. KW Heme; Oxygen transport; Transp; Erythrocyte. FT METAL 58 58 IRON (HEME DISTAL LIGAND). FT METAL 87 87 IRON (HEME PROXIMAL LIGAND). SQ SEQUENCE 141 AA; 15192 MW; 365EA7E98227347B CRC64;

Query Match 2.8%; Score 7; DB 1; Length 141; Best Local Similarity 100.0%; Pred. No. 11; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 VDDLPGA 202 Db 73 VDDLPGA 79

RESULT 11 HBA_SPEA ID HBA_SPEA STANDARD; PRT; 141 AA. DT 01-OCT-1989 (Rel. 12, Created) DT 01-NOV-1990 (Rel. 16, Last sequence update) DT 01-JUN-1994 (Rel. 29, Last annotation update) DE Hemoglobin alpha chain. OS Spermophilus parryi (Arctic ground squirrel) (Citellus parryi). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae; OC Spermophilus OC NCBI_TaxID=9999; RN [1] RP SEQUENCE. RX MEDLINE=87274834; PubMed=3608432; Duffy L.K., Ehrhardt M.M., Genaux C.T., Florant G.L.; "The primary structure of the hemoglobin alpha-chain of the arctic ground squirrel."; Comp. Biochem. Physiol. 87B:189-193(1987). DR PIR; JU0165; JU0165. DR HSSP; P01922; 1B20. DR InterPro; IPR002338; Alpha.haem. DR InterPro; IPR000971; Globin. DR Pfam; PF00042; globin; 1.

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DR EMBL; AE006762; AAK41693.1; ..
DR InterPro; IPR000816; Peptidase_C15.
DR Pfam; PF01470; Peptidase_C15; 1.
DR ProDom; PD008480; Peptidase_C15; 1.
DR PROSITE; PS01333; PYRASE_GLU; 1.
DR PROSITE; PS01334; PYRASE_CYS; 1.
KW Hydrolase; Thiol protease; Complete proteome.
FT ACT_SITE 79 79 BY SIMILARITY.
FT ACT_SITE 142 142 BY SIMILARITY.
FT ACT_SITE 164 164 BY SIMILARITY.
SQ SEQUENCE 211 AA; 23680 MW; 84416BE3CB745AB4 CRC64;

Query Match 2.8%; Score 7; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 TLGIGLA 22
|||||
DB 64 TLGIGLA 70

RESULT 15

FLPA_METVO
ID FLPA_METVO STANDARD; PRT; 228 AA.
AC P35553;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Fibrillarlin-like pre-rRNA processing protein.
GN FLPA OR RPPA.
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1537 / PS;
RX MEDLINE=94193565; PubMed=8144483;
RA Agha Amir K.;
RT "Fibrillarlin-like proteins occur in the domain Archaea.";
RL J. Bacteriol. 176:2124-2127(1994).
CC -!- FUNCTION: MAY BE INVOLVED IN PRE-RRNA PROCESSING.
CC -!- SIMILARITY: BELONGS TO THE FIBRILLARIN FAMILY.
CC
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DR EMBL; X73988; CAA52166.1; ..
DR PIR; S34646; S34646.
DR HSP; Q58108; 1FBN.
DR InterPro; IPR000692; Fibrillarlin.
DR Pfam; PF01269; Fibrillarlin; 1.
DR PRINTS; PR00052; FIBRILLARIN.
DR ProDom; PD004637; Fibrillarlin; 1.
DR PROSITE; PS00566; FIBRILLARIN; 1.
KW rRNA processing; rRNA-binding.
SQ SEQUENCE 228 AA; 25618 MW; 0AB2418DE0E324CF CRC64;

Query Match 2.8%; Score 7; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 134 LGASIIN 140
|||||

Db 57 LGASIIN 63

Search completed: October 30, 2002, 15:47:21
Job time : 13 secs

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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:46:05 ; Search time 27 Seconds
(without alignments)
1614.619 Million cell updates/sec

Title: US-09-910-033A-2
Perfect score: 252
Sequence: 1 MSNRLGKVAITGGTLGIG.....NESKFATGSEFVVDGGYTAQ 252

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	4.8	273	10 Q9SBM0	Q9sbm0 citrullus 1
2	10	4.0	247	2 Q93RM0	Q93rm0 acinetobact
3	10	4.0	251	2 Q9F7E0	Q9f7e0 acinetobact
4	10	4.0	260	16 Q9A326	Q9a326 caulobacter
5	9	3.6	250	5 O17721	O17721 caenorhabdi
6	9	3.6	267	10 P93697	P93697 vigna ungui
7	9	3.6	283	16 Q9A4H3	Q9a4h3 caulobacter
8	9	3.6	303	10 Q9SCU0	Q9scu0 arabidopsis
9	8	3.2	65	6 Q9TSA9	Q9tsa9 sus scrofa
10	8	3.2	65	6 Q9TSA2	Q9tsa2 sus scrofa
11	8	3.2	161	10 Q9LL33	Q9ll33 lycopersico
12	8	3.2	238	16 Q9HWL9	Q9hw19 pseudomonas
13	8	3.2	249	2 Q56841	Q56841 xanthobacte
14	8	3.2	250	2 Q937L4	Q937l4 comamonas t
15	8	3.2	251	10 Q40133	Q40133 lycopersico
16	8	3.2	251	16 Q98H76	Q98h76 rhizobium l

17	8	3.2	252	16 Q9KEC1	Q9kec1 bacillus ha
18	8	3.2	252	17 Q9YC43	Q9yc43 aeropyrum p
19	8	3.2	254	16 Q9A3X5	Q9a3x5 caulobacter
20	8	3.2	255	2 Q9ALP1	Q9alp1 saccharopol
21	8	3.2	256	2 Q93Q65	Q93qg5 brevivacter
22	8	3.2	256	16 Q92MR3	Q92mr3 rhizobium m
23	8	3.2	256	16 Q92MP6	Q92mp6 rhizobium m
24	8	3.2	257	16 Q92L02	Q92l02 rhizobium m
25	8	3.2	258	2 Q92NN8	Q92nn8 corynebacte
26	8	3.2	259	10 Q9LEG3	Q9leg3 lycopersico
27	8	3.2	259	10 Q93Y47	Q93y47 digitalis l
28	8	3.2	265	2 Q93S07	Q93s07 streptomyce
29	8	3.2	268	16 Q98LG1	Q98lg1 rhizobium l
30	8	3.2	269	3 Q96WJ1	Q96wj1 ophiostoma
31	8	3.2	272	10 Q9MLK9	Q9mlk9 arabidopsis
32	8	3.2	272	10 Q24452	Q24452 arabidopsis
33	8	3.2	276	2 Q93H71	Q93h71 streptomyce
34	8	3.2	276	11 Q08559	Q08559 rattus norv
35	8	3.2	276	13 Q90X71	Q90x71 anguilla ja
36	8	3.2	277	5 Q17726	Q17726 caenorhabdi
37	8	3.2	277	10 Q9SBD8	Q9sbd8 ipomoea tri
38	8	3.2	277	10 Q9SBD7	Q9sbd7 ipomoea tri
39	8	3.2	277	11 Q08558	Q08558 rattus norv
40	8	3.2	277	11 Q9JUN7	Q9j7n7 cricetus
41	8	3.2	277	11 Q91X28	Q91x28 mus musculu
42	8	3.2	278	10 Q94KL8	Q94kl8 podophyllum
43	8	3.2	281	10 Q42407	Q42407 silene lati
44	8	3.2	281	10 Q41345	Q41345 silene prat
45	8	3.2	284	10 Q82465	Q82465 ipomoea tri

ALIGNMENTS

RESULT 1

Q9SBM0 ID Q9SBM0 PRELIMINARY; PRT; 273 AA.
AC Q9SBM0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE WTS2L.
GN WTS2L.
OS Citrullus lanatus (Watermelon) (Citrullus vulgaris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
OX NCBI_TaxID=3654;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J., Kang H., Jun S., Lee J., An G.;
RT *Cloning of three gibberellin-regulated cDNAs from watermelon during
RT early seed development: down-regulated one cDNA and up-regulated two
RT cDNAs.*;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
CC EMEL; ABO18559; BAA89230.1; -.
CC HSP; P19992; LHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 273 AA; 28835 MW; 904A835DD52B6E2 CRC64;

Query Match 4.8%; Score 12; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RLDGKVAITGG 15
Db 12 RLDGKVAITGG 23

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RESULT 2
Q93RMO PRELIMINARY; PRT; 247 AA.
ID AC Q93RMO;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE CYCLOHEXANOL DEHYDROGENASE.
GN CHNA.
OS Acinetobacter sp. NCIMB9871.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=93373;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 9871;
RA Iwaki H., Hasegawa Y., Teraoka M., Tokuyama T., Lau P.C.;
RT "Identification and Characterization of Cyclohexanol Metabolic Genes
from Acinetobacter sp. NCIMB 9871."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026668; BAB61742.1;
SQ SEQUENCE 247 AA; 25657 MW; AB0DA7904DE726B3 CRC64;

Query Match 4.0%; Score 10; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 VHPGYIKTPL 195
| | | | | | | | | |
DB 185 VHPGYIKTPL 194

RESULT 3
Q9F7E0 PRELIMINARY; PRT; 251 AA.
ID AC Q9F7E0;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE CYCLOHEXANOL DEHYDROGENASE.
GN CHNA.
OS Acinetobacter sp. SE19.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=135835;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SE19;
RA Cheng Q., Thomas S.M., Kostichka K., Valentin J.R., Nagarajan V.;
RT "Genetic analysis of a gene cluster for cyclohexanol oxidation in
acinetobacter sp. strain SE19 by in vitro transposition."
RL J. Bacteriol. 182:4744-4751(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AF282240; AAG10026.1;
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 251 AA; 26159 MW; B5BAA48055997D5D CRC64;

Query Match 4.0%; Score 10; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 VHPGYIKTPL 195
| | | | | | | | | |
DB 189 VHPGYIKTPL 198

RESULT 4

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Q9A326 PRELIMINARY; PRT; 260 AA.
ID AC Q9A326;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE 2-DEOXY-D-GLUCONATE 3-DEHYDROGENASE.
GN CC3380.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RA MEDLINE=21173698; Pubmed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potočka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AE005999; AAK25342.1;
DR HSSP; P19992; IHDC.
DR TIGR; CC3380;
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 260 AA; 26992 MW; 96B83C46AB23E805 CRC64;

Query Match 4.0%; Score 10; DB 16; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 LAVNLGCVFF 120
| | | | | | | | | |
DB 116 LAVNLGCVFF 125

RESULT 5
Q17721 PRELIMINARY; PRT; 250 AA.
ID AC Q17721;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DE C55A6.6 PROTEIN.
GN C55A6.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kerahaw J.K.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; Pubmed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; Z81051; CAB02866.1;

```

RA Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.

AC Q9TSA9;


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DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PROTAGLANDIN 9-KETOREDUCTASE (EC 1.1.1.189) (FRAGMENTS).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92283276; PubMed=1597188;
RA Schieber A., Frank R.W., Ghisla S.;
RT "Purification and properties of prostaglandin 9-ketoreductase from pig
and human kidney. Identity with human carbonyl reductase.*";
RL Eur. J. Biochem. 206:491-502(1992).
FT NON_TER 1
FT NON_CONS 15 16
FT NON_CONS 30 31
FT NON_CONS 45 46
FT NON_CONS 56 57
FT NON_TER 65 65
SQ SEQUENCE 65 AA; 6922 MW; E821D57EE2001FAE CRC64;

Query Match 3.2%; Score 8; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
Db 8 LVNNAGIA 15

RESULT 10
Q9TSA2
ID Q9TSA2 PRELIMINARY; PRT; 65 AA.
AC Q9TSA2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PROTAGLANDIN 9-KETOREDUCTASE (EC 1.1.1.184) (FRAGMENTS).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=93081046; PubMed=1449827;
RA Schieber A., Ghisla S.;
RT "Prostaglandin 9-ketoreductase from pig and human kidney:
purification, properties and identity with human carbonyl reductase.*";
RL Eicosanoids 5:37-37(1992).
FT NON_TER 1
FT NON_CONS 15 16
FT NON_CONS 30 31
FT NON_CONS 45 46
FT NON_CONS 56 57
FT NON_TER 65 65
SQ SEQUENCE 65 AA; 6934 MW; 462F257EE2001FB2 CRC64;

Query Match 3.2%; Score 8; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
Db 8 LVNNAGIA 15

RESULT 11
Q9LL33
ID Q9LL33 PRELIMINARY; PRT; 161 AA.
AC Q9LL33;
DT 01-OCT-2000 (TReMBLrel. 15, Created)

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DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE LIGHT DEPENDENT NADH:PROTOCHLOROPHYLLIDE OXIDOREDUCTASE 3
DE (FRAGMENT).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RA Rubiera R., Neuhaus G.;
RT "Cloning of three putative light-dependent NADH:protochlorophyllide
oxidoreductases from Lycopersicon esculentum.*";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF243524; AAF82474.1;
FT NON_TER 1
FT NON_TER 161
SQ SEQUENCE 161 AA; 17286 MW; 5D1AB2EF071DBC6D CRC64;

Query Match 3.2%; Score 8; DB 10; Length 161;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 EKAASVG 52
Db 7 EKAASVG 14

RESULT 12
Q9HML9
ID Q9HML9 PRELIMINARY; PRT; 238 AA.
AC Q9HML9;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PROBABLE SHORT-CHAIN DEHYDROGENASE.
GN PA4162.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.*";
RL Nature 406:959-964(2000).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(CC) FAMILY
DR EMBL; AE004832; AGO7549.1;
DR HSSP; P50162; LAEI.
DR InterPro; IPR002198; ADH_short.
DR PRINTS; PR00080; SDRFAMILY.
KW Complete proteome: Oxidoreductase.
SQ SEQUENCE 238 AA; 24857 MW; 34643FA76B2B44CD CRC64;

Query Match 3.2%; Score 8; DB 16; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 LVNNAGIA 94
Db 73 LVNNAGIA 80

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RESULT 13

Q56841 PRELIMINARY; PRT; 249 AA.
 AC Q56841;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE ORF5 PROTEIN.
 GN ORF5.
 OS Xanthobacter sp.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Hypomicrobium group; Xanthobacter.
 OX NCBI_TaxID=35809;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PY2;
 RX MEDLINE-95219103; PubMed-7704278;
 RA Swaving J., Weljers C.A.G.M., van Ooyen A.J.J., de Bont J.A.M.;
 RT "Complementation of Xanthobacter Py2 mutants in epoxyalkane
 degradation: expression and nucleotide sequence of the complementing
 DNA fragment."
 RT Microbiology 141:477-484(1995).
 RL -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY: CAA56245.1;
 CC EMBL; X79863; CAA56245.1;
 DR HSP; P19992; IHDC.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
 KW Oxidoreductase.
 SQ SEQUENCE 249 AA; 24940 MW; B5E0B82C1D8D9782 CRC64;

Query Match 3.2%; Score 8; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 LVNNAGIA 94
 DB 82 LVNNAGIA 89
 |||||
 |||||

RESULT 14

Q937L4 PRELIMINARY; PRT; 250 AA.
 AC Q937L4;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE CYCLOHEXANOL DEHYDROGENASE (EC 1.1.1.1).
 GN CPMB.
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
 OX NCBI_TaxID=285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NCIMB 9872;
 RA van Beilen J.B., Fritsche U., Seeger M., Smits T.H.M., Witholt B.;
 RT "Cloning of Baeyer-Villiger monooxygenases from Comamonas,
 Xanthobacter and Rhodococcus via PCR with highly degenerate primers."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ418060; CAD10799.1;
 KW Oxidoreductase.
 SQ SEQUENCE 250 AA; 26626 MW; 7C42C3CBAEBB858E CRC64;

Query Match 3.2%; Score 8; DB 2; Length 250;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 VPDGVT 251
 DB 242 VPDGVT 249
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 |||||

RESULT 15

Q40133 PRELIMINARY; PRT; 251 AA.
 AC Q40133;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE ALCOHOL DEHYDROGENASE HOMOLOG (FRAGMENT).
 GN GAD3.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. MONEYMAKER;
 RX MEDLINE-96158488; PubMed-8580773;
 RA Jacobsen S.E., Olszewski N.E.;
 RT "Gibberellins regulate the abundance of RNAs with sequence similarity
 to proteinase inhibitors, dioxigenases and dehydrogenases."
 RL Planta 198:78-86(1996).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC EMBL; U21801; AAB00109.1;
 DR HSP; P29132; IDFI.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 KW Oxidoreductase.
 FT NON_TER 1
 SQ SEQUENCE 251 AA; 26202 MW; 8A6BCBDA15B90D53 CRC64;

Query Match 3.2%; Score 8; DB 10; Length 251;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GKVAITG 14
 DB 2 GKVAITG 9
 |||||
 |||||

Search completed: October 30, 2002, 15:48:34
 Job time : 29 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 20 Seconds
(without alignments)
1210.726 Million cell updates/sec

Title: US-09-910-033A-2
Perfect score: 1290
Sequence: I MSNLDGKVAITGGTIGIG.....NESKATGSEFVVDGGYTAQ 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	470	36.4	261	2	E87279		hypothetical prote
2	464.5	36.0	260	2	H70758		probable fabG3 pro
3	407.5	31.6	255	1	S10707		20beta-hydroxyster
4	400.5	31.0	255	1	S39737		glucose 1-dehydrog
5	393	30.5	254	2	S48129		3(or 17)beta-hydro
6	391	30.3	249	2	S47055		hypothetical prote
7	383	29.7	256	2	E72427		oxidoeductase, sh
8	380	29.5	247	2	E70740		probable fabG2 pro
9	374.5	29.0	248	2	F69868		glucose 1-dehydrog
10	372.5	28.9	253	2	B95284		probable [imported
11	371.5	28.8	261	2	J50385		glucose 1-dehydrog
12	370.5	28.7	261	2	A33528		glucose 1-dehydrog
13	368	28.5	253	2	B86737		acetoin dehydrogen
14	367	28.4	258	2	F70885		probable dehydroge
15	366	28.4	272	2	A59950		hypothetical prote
16	365.5	28.3	246	2	H72219		3-oxoacyl-(acyl ca
17	365.5	28.3	263	2	S01227		glucose 1-dehydrog
18	364.5	28.3	255	2	D70635		hypothetical prote
19	363.5	28.2	261	1	S00812		glucose 1-dehydrog
20	363	28.1	262	2	S02299		glucose 1-dehydrog
21	359	27.8	254	2	AD3182		short chain dehydr
22	358.5	27.8	261	2	D69629		glucose 1-dehydrog
23	357.5	27.7	251	2	A13185		dehydrogenase Atu5
24	357.5	27.7	258	2	D95284		probable [imported
25	357.5	27.7	261	2	I40225		glucose 1-dehydrog
26	357.5	27.7	271	2	EC0157		probable short cha
27	357	27.7	296	2	E87260		hypothetical prote
28	356.5	27.6	248	2	H98258		3-oxoacyl-(acyl-ca
29	356.5	27.6	248	2	A13025		3-oxoacyl1-(acyl-ca

ALIGNMENTS

RESULT 1

E87279

hypothetical protein CC0246 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C:Accession: E87279

R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; deBooy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kiro, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87279

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-261 <STO>

A:Cross-references: GB:AE005673; NID:gl3421377; PIDN:ANK22233.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC0246

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match	36.4%	Score 470;	DB 2;	Length 261;
Best Local Similarity	40.7%	Pred No. 4,1e-30;		
Matches 107;	Conservative 46;	Mismatches 90;	Indels 20;	Gaps 6;
QY	2	SNRLDGKVAITGGTIGIGLAITATFVEEGAKVMTDRHSVDGEKAASVGTDPDQIQ---	58	
Db	5	TGRVAGKAFITGGAGQGLGAAAGRLAKEGAKVAL---ADINLAGAQA--DEINAAH	58	
QY	59	-----FQHDSSDEGWTKLEDATEKAFGPVSTLVNNAAGIANKSVETTTAEWRKLLA	112	
Db	59	GAGTAFAFELDVTOEDQMDIVLEKATAAMGGLSVLVNNAIGDGPISLDFGLMKVMS	118	
QY	113	VNLDCVFCTRIGIORMKNKLGASIIINSSIEGVPDPSLGAYNASKAGVIMSKSAAL	172	
Db	119	VNVDVFLGAKHALTHMAHQPG-SIINLSSTAGLIANGSNPAYNASKAAVLLSKNIAL	177	
QY	173	DCALKDYDVRVNVHPGIKTPLVDDLP---GAERAMSORTK-TPMGHIGEPNDIAYICV	228	
Db	178	YCAKMKLDIRSNSIHPTFTIDTPILDGFSARFGKEAFARQVPLGRIGEPDTIANAVL	237	
QY	229	YLASNEKFAFGSEFVVDGGYTA	251	
Db	238	YLASDESKFMTGAEIKVDGGISA	260	

RESULT 2

H70758

probable fabG3 protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: H70758

R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A: Authors: Soares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
 A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A: Reference number: A70500; MUID: 98295987
 A: Accession: H70758
 A: Status: preliminary; nucleic acid sequence not shown; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-260 <COL>
 A: Cross-references: GB:Z74025; GB:AL123456; NID: g3261586; PIDN: CAA98414.1; PID: g3261591
 A: Experimental source: strain H37RV
 C: Genetics:
 C: Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F: 8-184/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 36.0%; Score 464.5; DB 2; Length 260;
 Best Local Similarity 42.2%; Pred. No. 1.1e-29;
 Matches 106; Conservative 44; Mismatches 90; Indels 11; Gaps 5;

QY 1 MSNRDGVKVAITGGTGLGATATKFFVEGAKVMTDRHSDVGEKAASVGTDPQIQFF 60
 DB 1 MSGRLLGKVALVSGGARGMGASHVRAWAGKVFGLDDEGKAAVAELA--DAARYV 58
 QY 61 QHDSDEDEGWTKLFDATKAFGVPSTLVNNAIVNAGVSVETTTAEWRKLLAVNLGCVFF 120
 DB 59 HLDVTPQAQWTAADVAFTAGGLHVLVNNAGILNTIGTIEDYALTEWQRLDVLNIGVFL 118

QY 121 GTRLGTRQMKNGKGLGASIISSIEGFGDPSLGAYNASKGAVRIMSKSAALCALDKYD 180
 DB 119 GIRAVYKPKKEARGC-SIINISIEGLAGTVACHGYTATKFAVRGLTKSTALE--LGP 175

QY 181 VRVNTVHPGYIKTPLVDLPGAEAMRSQRTKTPMGHIGPNDAICVYLASNESKATG 240
 DB 176 IRVNSHPLGLVTPWTDVNP--EDIF---QALGRAAEPEVSNLVVILASDESISTG 229

QY 241 SEFVWDGGYTA 251
 DB 230 AEFVWDGGTVA 240

RESULT 3
 S10707
 20beta-hydroxysteroid dehydrogenase (EC 1.1.1.-) - Streptomyces exfoliatus
 C: Species: Streptomyces exfoliatus
 C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A: Accession: S10707

R: Marekov, L.; Krook, M.; Joernvall, H.
 FEBS Lett. 266, 51-54, 1990
 A: Title: Prokaryotic 20-beta-hydroxysteroid dehydrogenase is an enzyme of the 'short-chain' alcohol dehydrogenase family
 A: Reference number: S10707; MUID: 90306362
 A: Accession: S10707

A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 1-255 <MAR>
 C: Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C: Keywords: NAD; oxidoreductase
 F: 7-183/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 31.6%; Score 407.5; DB 1; Length 255;
 Best Local Similarity 39.0%; Pred. No. 3.8e-25;
 Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;

QY 3 NRDLGKVAITGGTGLGATATKFFVEGAKVMTDRHSDVGEKAASVGTDPQIQFF 62
 DB 2 NDLGKVTIITGGTGLGAEAAQAAVAVVAVLADVLDEGAATAARELG--DAARYQL 59

QY 63 DSSDEDEGWTKLFDATKAFGVPSTLVNNAIVNAGVSVETTTAEWRKLLAVNLGCVFF 122
 DB 60 DVTIEDQRVAVAREEFGVDGLVNNAGISTGMFLETESVERFRKVVYDINLTGTFIGM 119

QY 123 RLGIQRMKNKGLGASIISSIEGFGDPSLGAYNASKGAVRIMSKSAALCALDKYDVR 182
 DB 120 KTVIPAMKQAG-GGSIVNISSAAGLMLATSSYGASKGVRGLSKLAAVE--LCGDRIR 176
 QY 183 VNTVHPGYIKTPLVDLPGAEAMRSQRTKTPMGHIG-EPNDIAYICVYLASNESKATG 241
 DB 177 VNSVHPGWTYTPMTAE-TGIRQEGNYPNTPMGVRGNEPEIAGAVVKLLSDTSSVYVTA 235
 QY 242 EFWVDGGYT 250
 DB 236 ELAVDGGWT 244

RESULT 4

S39737

glucose 1-dehydrogenase homolog ywfd - Bacillus subtilis

N: Alternate names: protein ipa-82d

C: Contains: probable dehydrogenase (EC 1.1.1.-)

C: Species: Bacillus subtilis

C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C: Accession: S39737; E70055

R: Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionec

A: A.; Rapoport, G.; Danchin, A.

Mol. Microbiol. 10, 371-384, 1993

A: Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb regic

A: Reference number: S39655; MUID: 95020537

A: Accession: S39737

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-255 <GLA>

A: Cross-references: EMBL: X73124; NID: g413923; PIDN: CAA51638.1; PID: g414006

A: Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1993

R: Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be

C.: Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.: Ehrlich, S.D.; Emmerson, P.F.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari,

Nature 390, 249-256, 1997

A: Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Ga

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo,

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardir

A: Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scan

A: Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; S

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy

T.; Winters, P.; Wipat, A.; Yamamoto, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshic

A: Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtil

A: Title: The complete genome sequence of the Gram-positive bacterium

A: Reference number: A69580; MUID: 98044033

A: Accession: E70055

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-255 <KUN>

A: Cross-references: GB:Z99123; GB:AL009126; NID: g2636240; PIDN: CAB15799.1; PID: g2636

A: Experimental source: strain 168

C: Genetics:

C: Gene: ywfd

C: Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C: Keywords: NAD; oxidoreductase

F: 8-185/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 31.0%; Score 400.5; DB 1; Length 255;
 Best Local Similarity 37.1%; Pred. No. 1.4e-24;
 Matches 96; Conservative 45; Mismatches 107; Indels 11; Gaps 6;

QY 1 MSNRDGVKVAITGGTGLGATATKFFVEGAKVMTDRHSDVGEKAASVGTDPQIQFF 60

DB 1 MIMNLTDKTVLTITGASGIGYAAVQAFGLQQAQNVVADIDEAQGEAMVRKNN-DRHFV 59

QY 61 QHDSDEDEGWTKLFDATKAFGVPSTLVNNAIVNAGVSVETTTAEWRKLLAVNLGCVFF 120

DB 60 QTDITDEAACQHAVESAVHTFGDLVNLNAGIEYIPIHEMELSDNKNVQLVNLGML 119

QY 121 GTRLGTRQMKNGKGLGASIISSIEGFGDPSLGAYNASKGAVRIMSKSAALCALDKYD 180

Db 120 MSKHALKMLAAGK-NIINTSVGLVAMPDIPAYNASKGVQLQTLTKSMAYDYA--KHQ 176
QY 181 VRVTVHPGKIYKTP-----VDLPGA-EEAMSORTK-TPMGHIGEPNDIAICVYLASN 233
Db 177 IRVNCVCPGIDTPLNEKSFLENNGTLEEIKKAKVNPLRLKGPBEIANVMLFLASD 236
QY 234 ESKFATGSEFVVGGYTAQ 252
Db 237 LSSYMTGSAITADGGYTAQ 255
RESULT 5
S48129
3(or 17)beta-hydroxysteroid dehydrogenase (EC 1.1.1.51) - Comamonas testosteroni (ATCC 1
C:Species: Comamonas testosteroni
A:Variety: ATCC 11996
C:Date: 14-Jul-1995 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999
C:Accession: S48129; S51780; S15390; S62216; S62182
R:Abalain, J.H.; di Stefano, S.; Anet, Y.; Quemener, E.; Abalain-Colloc, M.L.; Floch, H.
J. Steroid Biochem. Mol. Biol. 44, 133-139, 1993
A:Title: Cloning, DNA sequencing and expression of (3-17)beta-hydroxysteroid dehydrogena
A:Reference number: S48129; MUID:93176721
A:Accession: S48129
A:Molecule type: DNA
A:Residues: 1-254 <ABA>
A:Cross-references: EMBL:X63379
A:Note: The source is designated as Pseudomonas testosteroni
R:Abalain, J.H.
submitted to the EMBL Data Library, November 1991
A:Reference number: S51780
A:Accession: S51780
A:Molecule type: DNA
A:Residues: 1-13, 'VV', 16-254 <ABW>
A:Cross-references: EMBL:X63379; NID:g312918; PIDN:CAA44977.1; PID:g312919
A:Note: the source is designated as Pseudomonas testosteroni
R:Yin, S.J.; Vagelopoulos, N.; Lundquist, G.; Joernvall, H.
Eur. J. Biochem. 197, 359-365, 1991
A:Title: Pseudomonas 3-beta-hydroxysteroid dehydrogenase. Primary structure and relation
A:Reference number: S15390; MUID:91224127
A:Accession: S15390
A:Molecule type: protein
A:Residues: 2-40, 'E', 41-176, 178-240, 'G', 242-254 <YN>
A:Note: The source is designated as Pseudomonas testosteroni
R:Benach, J.; Knapp, S.; Oppermann, U.C.T.; Haegglund, O.; Joernvall, H.; Ladenstein, R.
Eur. J. Biochem. 236, 144-148, 1996
A:Title: Crystallization and crystal packing of recombinant 3 (or 17) beta-hydroxysteroid
A:Reference number: S62216; MUID:96184891
A:Accession: S62216
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 2-254 <BEN>
R:Bocco, J.L.; Panzetta, G.; Actis, L.A.; Genti-Raimondi, S.
submitted to the EMBL Data Library, July 1993
A:Description: Nucleotide sequence of the beta-hydroxysteroid dehydrogenase from Pseudom
A:Reference number: S62182
A:Accession: S62182
A:Molecule type: DNA
A:Residues: 1-40, 'E', 41-176, 178-254 <BOC>
A:Cross-references: EMBL:L08971; NID:g309859; PIDN:AAA25742.1; PID:g309860
A:Note: The source is designated as Pseudomonas testosteroni
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:2-254/Product: 3(or 17)beta-hydroxysteroid dehydrogenase #status experimental <MAT>
F:8-185/Domain: short-chain alcohol dehydrogenase homology <SADH>
Query Match 30.5%; Score 393; DB 2; Length 254;
Best Local Similarity 36.7%; Pred. No. 5.4e-24;
Matches 92; Conservative 49; Mismatches 100; Indels 10; Gaps 6;
QY 1 MSNRLDGKVAITGGTIGLIGLAIATKFFVEGAKVMITDRHSDVGEKAASVGTDPDQIOFF 60
Db 1 MTRNLQKRVALTGSGAGVEVYKLLIGEGAKVAFSDINA-AGQQLAAELG--ERSNFV 57

QY 61 QHDSDEDCWTKLFDATEKAFGVPSTLVNAGIYANKSVSEETTAEWRKLLAVNLGVFF 120
Db 58 REDVSEADTWLVMAVORRLGTILVNVNAGILLPGDMETGRLEDFSRLLKINTESVFI 117
QY 121 GYRLGIQRMKNGKLGASIIINSSIEFGVDPGLSGLAYNASKGAVRIMSKAALDCAKDYD 180
Db 118 GCQOQIAAMKE--TGSIINMASVSWLPFIEQVAGYSASKAAVSALTAAALSCRRQGYA 175
QY 181 V-RVNTVHPGIYKTPLYD-DLP---GAERAMSQRKTPMGHIGEPNDIAICVYLASNES 235
Db 176 IRRVNSIHPDGIYTPMQOASLPKGVSKEMVLHDPKLNLRAGRAYMPEIRIAQLVFLASDES 235
QY 236 KEATGSEFVVD 246
Db 236 SVMSGSELHAD 246
RESULT 6
S47055
hypothetical protein 5 - Xanthobacter sp.
C:Species: Xanthobacter sp.
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
R:Swaving, J.; Weijers, C.A.G.M.; van Ooyen, A.J.J.; de Bont, J.A.M.
submitted to the EMBL Data Library, June 1994
A:Description: Plenmentation of Xanthobacter Py2 mutants in epoxyalkane degradation; e
A:Reference number: S47051
A:Accession: S47055
A:Molecule type: DNA
A:Residues: 1-249 <SWA>
A:Cross-references: EMBL:X79863; NID:g520947; PIDN:CAA56245.1; PID:g520952
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F:5-181/Domain: short-chain alcohol dehydrogenase homology <SADH>
Query Match 30.3%; Score 391; DB 2; Length 249;
Best Local Similarity 38.9%; Pred. No. 7.6e-24;
Matches 98; Conservative 39; Mismatches 105; Indels 10; Gaps 6;
QY 5 LDGKVAITGGTIGLIGLAIATKFFVEGAKVMITDRHSDVGEKAASVGTDPDQIOFFQHDS 64
Db 2 LDAEVIAITGGAGIGLAVAHAAIRAGARVALIDRDGACAOQRAAEFGA--AAWGVGADV 59
QY 65 SDEDCWTKLFDATEKAFGVPSTLVNAGIYANKSVSEETTAEWRKLLAVNLGVFFGTSL 124
Db 60 TDEAAITAAAGAQALGPLTGLVNVNAGIYANKSVSEETTAEWRKLLAVNLGVFFGTSLASKA 119
QY 125 GIQRMKNGKLGASIIINSSIEFGVDPGLSGLAYNASKGAVRIMSKAALDCAKDYDVVN 184
Db 120 ALFGMLERGRGA-IVNFGSVAGLVGIPDMAAYCAKAGAVNLTROMAADYSGR--GIRVN 176
QY 185 TVHPGIYK-TPLVDDLPAGE---EAMSOR-TKTPMGHIGEPNDIAICVYLASNESKFAT 239
Db 177 VVCPGTAVAGTDMGROLLGTDCDPELEARRLAKYPMGRFGTPEIDIAEAFAVLLSTKAAFT 236
QY 240 GSEFVVDGSGYTA 251
Db 237 GSVLAVDGGMTA 248
RESULT 7
E72427
oxidoreductase, short chain dehydrogenase/reductase family - Thermotoga maritima (str
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: E72427
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: E72427

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <ARN>

A:Cross-references: GB:AE001690; GB:AE000512; NID:94980496; PIDN:AAD35113.1; PID:9498050

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0019

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 29.7%; Score 383; DB 2; Length 256;

Best Local Similarity 35.5%; Pred. No. 3.4e-23;

Matches 93; Conservative 48; Mismatches 95; Indels 26; Gaps 7;

QY 5 LDKKVAITGGTIGLAIATKFEVGEAKVMTDRHSDVG---EKAASKVGTDPDQIOFFQ 61

Db 2 LEKKVAVVTGGGCGIGAAIAQLAENGMKVIVIAEIDEAGVEREEMLRERGL--DVTFFK 59

QY 62 HDSDSDGWTKLFDATEKAFGPVSTLVNNAIVNKSVEETTAWEKLLAVNLGDVFFG 121

Db 60 TVADENSVMKVRKTVIEYGGVDLVNNAVMSVKSFIFERPLEEWEKRVIRNLTGPYIC 119

QY 122 TRGLIQRMKNKGLGASIIINSSIEGFGDPSLGAYNASKGAVRIMSKSAALDCALKDYDV 181

Db 120 SRYCAEEMIKRG-GGVIIINASTRAFOSEPTDPYSASKGLVATHSLAV--SLSYHI 176

QY 182 RVNTVHPGYIKTPLVDLPQAEAMSOQTKT-----PMGHIGEPNDIAYICVYL 231

Db 177 RVVISIPGWJET-----SEMKKSLRKKPDLRPIDHEQHPAGRVGNPLDIAHLCVFLA 229

QY 232 SNE-SKPFATGSEFVVDGGYTAQ 252

Db 230 DDEKAGFYGTNFIVDGGMVTK 251

RESULT 8

E70740

probable fabc2 protein - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

A:Accession: E70740

R:Cole, S.T.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

R:Connor, R.; Blos, K.; Devlin, K.; Reltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

R:Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987

A:Accession: E70740

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-247 <COL>

A:Cross-references: GB:Z75555; GB:AL123456; NID:93261608; PIDN:CAA99983.1; PID:91419053

A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: fabG2

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F:8-186/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 29.5%; Score 380; DB 2; Length 247;

Best Local Similarity 36.2%; Pred. No. 5.7e-23;

Matches 92; Conservative 52; Mismatches 94; Indels 16; Gaps 4;

QY 1 MSNRLDGKVAITGGTIGLAIATKFEVGEAKVMTDRHSDVGGEAKKSVGTPDQIOFF 60

Db 1 MASLLNARTAVITGGAGGGLGAIQRFVAGARVLDVNLATEVAARLGGDDVALAV 60

QY 61 QHSDSDGWTKLFDATEKAFGPVSTLVNNAIVNKSVEETTAWEKLLAVNLGDVFF 120

Db 61 RCDVTQADDVDLIRTFVAFERFGLDVMVNNAGITRDATMTTTEQFDQVIAHLKGTWN 120

QY 121 GTRLGIQRMKNKGLGASIIINSSIEGFGDPSLGAYNASKGAVRIMSKSAALDCALKDYDV 180

Db -121 GT-LAAAIHRRKRG-IVNNSVSGKVGWGTQNTYSAAGAGIVGMTKAAAKE--LAHLG 177

QY 181 VRVNTVHPGYIKTPLVDLPQAEAMSOQ-----TKTPMGHIGEPNDIAYICVYLASNE 234

Db 178 IRVNAIAPGLIRSAMT-----EAMPQIWDQKLAIEVPMGRAGEPSEVASVAVFLASDL 230

QY 235 SKPFATGSEFVVDGG 248

Db 231 SSYMTGTVDLTG 244

RESULT 9

F69868

glucose 1-dehydrogenase homolog ykvo - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

A:Accession: F69868

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; B.

C.: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.

A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari.

Nature 390, 249-256, 1997

A:Authors: Fulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; G.

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo,

Kostter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardir

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scar

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.;

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchi

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshi

A:Authors: Yoshikawa, H.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil

A:Reference number: A69580; MUID:98044033

A:Accession: F69868

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-248 <KUN>

A:Cross-references: GB:Z99111; GB:AL009126; NID:92633699; PIDN:CAB13250.1; PID:9263

A:Experimental source: strain 168

C:Genetics:

A:Gene: ykvo

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

F:7-182/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 29.0%; Score 374.5; DB 2; Length 248;

Best Local Similarity 37.5%; Pred. No. 1.6e-22;

Matches 93; Conservative 40; Mismatches 106; Indels 9; Gaps 5;

QY 4 RLDGKVAITGGTIGLAIATKFEVGEAKVMTDRHSDVGGEAKKSVGTPDQIOFFQHD 63

Db 3 KFEKIALVTGGTIGLAIATKFEVGEAKVMTDRHSDVGGEAKKSVGTPDQIOFFQHD 60

QY 64 SDESDGWTKLFDATEKAFGPVSTLVNNAIVNKSVEETTAWEKLLAVNLGDVFFGTR 123

Db 61 ISKLEDDKLDYIKQEKGLDILFANAGNPLFGEITEEQVDRTFIDNVKGTFTVQ 120

QY 124 LGTQRMKNKGLGASIIINSSIEGFGDPSLGAYNASKGAVRIMSKSAALDCALKDYDV 183

Db 121 KALSFPDK--VGSIIIVTGTAGSIGNPAFVYGAASKAALRALVRWILD--LKGTEIRV 176

QY 184 NTVHPGYIKTPLVDLPQAEAMSOQTKT-----PMGHIGEPNDIAYICVYLASNEKFATG 240

Db 177 NVVSPGILTPAYDELFGDALEVLNSRNTVPAGKVGTPPEEVANAVSFLASDESSTLTG 236

QY 241 SEFVVDGG 248

Db 237 VELFVDGG 244

RESULT 10

B95284

probable [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

[illegible]

```

Query Match      28.8%; Score 371.5; DB 2; Length 261;
Best Local Similarity 34.2%; Pred. No. 2.9e-22;
Matches 86; Conservative 51; Mismatches 102; Indels 13; Gaps

Qy   1 MSNRLDGKVAIIIGTGLIGLATATKFVEEGAKVMTIDRHSDVGKA-----AKSVGTP 54
    | :||| :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   1 MYKDEGVVVITGSSTGLGKSWAIFATEKAKVVVYRSKE--EANSVLEEIKKVGE 56
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   55 DOIQFOHDSDEDGWTKLFDATEKAFGPVSTLVNNAGIANKVSVEETTTAEWRKLLAVN 114
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   57 GEATAVGDDVTESDVNLVVOSSIKEFGKLDVMINNAGMENPVSSHMSLSDWNKVIDTN 116
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   115 LDGVFFGRLGIOBMKNKGILGASLIINMSIEFVGDPSPSGAYNASKGAVRIMSKSAALDC 174
    | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   117 LTGAFLGREAIFYENDIKGVIVNMSSVHEKIPMLPFVHYAAASKGGMKLTETLALEY 176
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   175 ALKDYDVRNVTHPGVIKTPL-VDDLPGAEEAMSORTKPMGHIGEPNNDIAVICVYLASN 233
    | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   177 APK--GIRVNNGIGAINTPINAEEKPADPEORADVESMIPMGYIGEPEEIAVAANWASS 234
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   234 ESKFATGSEFFVDGGYT 250
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   235 EASYVTGITLFDAGGMT 251
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 12
A33528
glucose, l-dehydrogenase (EC 1.1.1.47) - Bacillus megaterium
C:Species: Bacillus megaterium
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 11-Jun-1999
C:Accession: A33528
R:Makino, Y.; Negoro, S.; Urabe, I.; Okada, H.
J. Biol. Chem. 264, 6391-6395, 1989
A:Title: Stability-Increasing mutants of glucose dehydrogenase from Bacillus
A:Reference number: A33528; MUID:89197943
A:Accession: A33528
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <MAK>
A:Cross-references: GB:J04805; NID:g142974; PIDN:AAA22475.1; PID:g142975
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase hom
C:Keywords: oxidoreductase
F:8-189/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match      28.7%; Score 370.5; DB 2; Length 261;
Best Local Similarity 33.6%; Pred. No. 3.5e-22;
Matches 86; Conservative 51; Mismatches 108; Indels 11; Gaps

Qy   1 MSNRLDGKVAIIIGTGLIGLATATKFVEEGAKVMT-----DRHSDVGKAAKSVGTPD 55
    | :||| :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   1 MYKDEGVVVITGSSTGLGKSWAIFATEKAKVVVYRSKEDEANSVLEEIKKVGEAI 60
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   56 QIOFQHDSSDEDGWTKLFDATEKAFGPVSTLVNNAGIANKVSVEETTTAEWRKLLAVNT 115
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   61 AV---KGDVTVESDVNLVQSAAIKFEFKLDVMINNAGLENVPSSHMSLSDWNKVIDTNL 117
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   116 DGVFFGRLGIOBMKNKGILGASLIINMSSTIEGFVGDPSPSGAYNASKGAVRIMSKSAALDCA 175
    | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   118 TGAF LGREAIFYENDIKGVIVNMSSVHEKIPMLPFVHYAAASKGGMKLTETLALEYA 177
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   176 LKDYDVRNVTHPGVIKTPL-VDDLPGAEEAMSORTKPMGHIGEPNNDIAVICVYLASN 234
    | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   178 PK--GIRVNNGIGAINTPINAEEKPADPEORADVESMIPMGYIGEPEEIAVAANWASS 235
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy   235 SKFATGSEFFVDGGYT 250
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db   236 ASYVTGITLFDAGGMT 251
    : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

```

RESULT 13
B86737
acetoin d

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 12 Seconds
(without alignments)

813.111 Million cell updates/sec

Title: US-09-910-033A-2

Perfect score: 1290

Sequence: 1 MSNRLDGKVAITGTGIG.....NESKATGSEFVVDGGYTAQ 252

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	464.5	36.0	260	1 YK02_MYCTU	Q10855 mycobacteri
2	441.5	34.2	250	1 LINC_PSEPA	P50198 pseudomonas
3	407.5	31.6	255	1 2BHD_STREX	P19992 streptomyce
4	400.5	31.0	255	1 YWFD_BACSU	P39640 bacillus su
5	383	29.7	256	1 Y019_THEMEA	Q56318 thermotoga
6	380	29.5	247	1 YD50_MYCTU	Q11020 mycobacteri
7	371.5	28.8	261	1 DHG1_BACME	P39482 bacillus me
8	370.5	28.7	261	1 DHG2_BACME	P40288 bacillus me
9	370	28.7	253	1 3BHD_COMTE	P19871 comamonas t
10	365.5	28.3	246	1 FABG_THEMEA	Q9x248 thermotoga
11	363.5	28.2	261	1 DHGA_BACME	P10528 bacillus me
12	360	27.9	262	1 DHGB_BACME	P07999 bacillus me
13	358.5	27.8	261	1 DHG_BACSU	P12310 bacillus su
14	357.5	27.7	261	1 DHG4_BACME	P39485 bacillus me
15	355.5	27.6	261	1 DHG2_BACME	P39483 bacillus me
16	352.5	27.3	261	1 DHG3_BACME	P39484 bacillus me
17	351.5	27.2	251	1 Y325_THEMEA	Q9wyq0 thermotoga
18	348.5	27.0	258	1 DHG2_BACSU	P80869 bacillus su
19	345	26.7	261	1 DHB2_HUMAN	Q92506 homo sapien
20	339.5	26.3	256	1 BUDC_KLEPN	Q48436 klebsiella
21	326	25.3	285	1 G539_BACSU	P80873 bacillus su
22	325.5	25.2	260	1 DHB8_MOUSE	P50171 mus musculu
23	324	25.1	336	1 TS2_WAIZE	P50160 zea mays (m
24	322	25.0	289	1 YHDF_BACSU	Q07575 bacillus su
25	321	24.9	248	1 FABG_CHLMU	Q9pkf7 chlamydia m
26	321	24.9	548	1 YAVI_RHISN	Q53217 rhizobium s
27	319.5	24.8	256	1 GNO_GLUOX	P50199 gluconobact
28	319.5	24.8	258	1 BDHA_RHIME	Q86034 rhizobium m
29	318	24.7	244	1 FABG_VIBCH	Q8kq7 vibrio chol
30	317.5	24.6	262	1 VER1_ASPPA	P50161 aspergillus
31	317	24.6	241	1 PHBB_ZOORA	P32338 zoogloea ra
32	316	24.5	246	1 FABG_BACSU	P51831 bacillus su
33	316	24.5	281	1 SOUL_CANAL	P87219 candida alb

34	313.5	24.3	264	1 STCU_EMENI	Q00791 emericeila
35	312	24.2	241	1 PHBB_RHIME	P50205 rhizobium m
36	312	24.2	248	1 FABG_AQUAE	O67610 aquifex aeo
37	310.5	24.1	271	1 SDRL_PICAB	Q08632 picea abies
38	310	24.0	273	1 TRNL_DATST	P50162 datura stra
39	307.5	23.8	250	1 LINC_PSEPA	P50197 pseudomonas
40	305	23.6	247	1 FABG_CHLFR	P38004 chlamydia t
41	305	23.6	285	1 YHXC_BACSU	P40397 bacillus su
42	304.5	23.6	248	1 FABG_CHLPN	Q9z8p2 chlamydia p
43	303	23.5	278	1 YALA_RHISN	P55541 rhizobium s
44	301.5	23.4	320	1 FABG_CUPLA	P28643 cuphea lanc
45	299.5	23.2	253	1 Y4MP_RHISN	P55575 rhizobium s

ALIGNMENTS

RESULT 1
YK02_MYCTU
ID YK02_MYCTU STANDARD; PRT; 260 AA.
AC Q10855;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase RV2002 (EC 1.-.-.-).
GN FABG3 OR RV2002 OR MT2058 OR MTCY39.16C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID:1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:H37RV;
RX MEDLINE:98295987; PubMed:9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN:CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishal W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
CC EMBL; Z4025; CAA98414.1; --
CC EMBL; AE007057; AAK46335.1; --
CC HSSP; P19992; 1HDC.
CC TIGR; MT2058; --
CC TubercuList; RV2002; --
CC InterPro; IPR002198; ADH_short.

```

DR PFam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
FT NP_BIND 11 35 NAD (BY SIMILARITY).
FT ACT_SITE 153 153 BY SIMILARITY.
FT CONFLICT 174 174 S->G (IN REF. 2).
SQ SEQUENCE 260 AA; 27030 MW; 0935A14ED36220B7 CRC64;

Query Match 36.0%; Score 464.5; DB 1; Length 260;
Best Local Similarity 42.2%; Pred. No. 6.6e-31;
Matches 106; Conservative 44; Mismatches 90; Indels 11; Gaps 5;

QY 1 MSNRDQKVAITGGTIGIGLATATKFEVGEKAVMTDRSDVGEKAASVGPDPQIQFF 60
DB 1 MSGRLLKVALVSGGAGMASHVRAMVGEKAVVFGDILDEEGKAVAAELA--DAARYV 58
QY 61 QHSDSDGWTGKLFDATEKAFGPVSTLVNNAIYVKNKSVETTTAEWRKLLAVNLDGVFF 120
DB 59 HLDVTPQAQVAADVAVTAFGLHLVNNAGILNIGTIEDYALTEQRIIDVNLGTGVL 118
QY 121 GTRIGIORMKNGKLGASIIINSSIEGTFVGPDSLGAYNASKGAVRIMSKSAALDKDYD 180
DB 119 GIRAVKPKMEAGRG-SIINSSIEGLAGTVAGCHGYATATKFAVRGLTKSTALE--LPSG 175
QY 181 VRYVTHVPGIKPLVDLPCAEAMSQRTKTPMGHIGEPNDIAYICVYLASNEKSFATG 240
DB 176 IRVNSIHPLGKVTMTDWP--EDIF---QTALGRAAEPEVSNLVVYLASDESSYSTG 229
QY 241 SEFVVDGGTVA 251
DB 230 AEFVVDGGTVA 240

RESULT 2
LINK_PSEPA
ID LINK_PSEPA STANDARD; PRT; 250 AA.
AC P50198;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)
GN LINK.
OS Pseudomonas paucimobillis (Sphingomonas paucimobillis).
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC Sphingomonas.
OX NCBI_TaxID=13689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UT26;
RX MEDLINE=94252977; PubMed=7515041;
RA Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
RT "Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
RT dehydrogenase gene involved in the degradation of gamma-
RT hexachlorocyclohexane in Pseudomonas paucimobillis.";
RL J. Bacteriol. 176:3117-3125(1994).
CC -!- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
CC (2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DCHO). LINK IS NOT
CC ESSENTIAL TO GAMMA-HCH DEGRADATION.
CC -!- PATHWAY: DEGRADATION OF GAMMA-HEXACHLOROCYCLOHEXANE.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D23722; BAA04939.1;

DR HSSP: P19992; LHDC.
DR InterPro: IPR002198; ADH_short.
DR PFam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NP_BIND 9 34 NAD (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 250 AA; 25492 MW; 8C52703FF76382CF CRC64;

Query Match 34.2%; Score 441.5; DB 1; Length 250;
Best Local Similarity 41.0%; Pred. No. 4.7e-29;
Matches 105; Conservative 43; Mismatches 93; Indels 15; Gaps 6;

QY 1 MSNRDQKVAITGGTIGIGLATATKFEVGEKAVMTDRSDVGEKAASV-----GTPD 55
DB 1 MANRLAGKVALITGGASGLGAQAQKRAEAGKAVI---GDLNEEMAKGVVAEIRAAG 56
QY 56 QIOFFHSDSDGWTGKLFDATEKAFGPVSTLVNNAIYVKNKSVETTTAEWRKLLAVN 115
DB 57 DALFRLDVTDAASWNAIAAAYDVGGLTTLNTAGIHPGGFEESIEGWNKMWAVNQ 116
QY 116 DGVFFGTRIGIORMKNGKLGASIIINSSIEGTFVGPDSLGAYNASKGAVRIMSKSAALDCA 175
DB 117 TAIFLAGTKAAIPELVKSGNG-SIINSSIEGLMFTAGNASYCATKAAVRIMSKAAALE-- 173
QY 176 LKDYDVRYVTHVPGIKPLVDLPCAEAMSQRTKTPMGHIGEPNDIAYICVYLASNE 234
DB 174 FVDRGVRYVTHVPGMNTPTITANVP--PDVLKQOTSQIPMGKLGDPIDIANGLFLASDE 231
QY 235 SKFATGSEFVVDGGYT 250
DB 232 AKYITGVLDLPIDGWS 247

RESULT 3
2BHD_STREX
ID 2BHD_STREX STANDARD; PRT; 255 AA.
AC P19992;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 20-beta-hydroxysteroid dehydrogenase (EC 1.1.1.53).
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RX MEDLINE=90306362; PubMed=2194840;
RA Marekov L., Krook M., Joernvall H.;
RT "Prokaryotic 20 beta-hydroxysteroid dehydrogenase is an enzyme of the
RT 'short-chain, non-metalloenzyme' alcohol dehydrogenase type.";
RL FEBS Lett. 266:51-54(1990).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RP MEDLINE=92052211; PubMed=1946424;
RA Ghosh D., Weeks C.M., Grochulski P., Duax W.L., Erman M.,
RA Rimsay R.L., Orr J.C.;
RT "Three-dimensional structure of holo 3 alpha,20 beta-hydroxysteroid
RT dehydrogenase: a member of a short-chain dehydrogenase family.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10064-10068(1991).
CC -!- CATALYTIC ACTIVITY: Androstan-3-alpha,17-beta-diol + NAD(+) -> 17-
CC beta-hydroxyandrostan-3-one + NADH.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC PIR: S10707; S10707.
CC PDB: 2HSD; 3I-AUG-94.
CC PDB: LHDC; 07-FEB-95.
CC InterPro: IPR002198; ADH_short.
CC PFam: PF00106; adh_short; 1.
CC PRINTS: PR00080; SDRFAMILY.

```

```

DR PRINTS: PRO0080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
SQ ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 255 AA; 27324 MW; 20AA2259BF88C9B CRC64;

Query Match
Best Local Similarity 31.0%; Score 400.5; DB 1; Length 255;
Matches 96; Conservative 45; Mismatches 107; Indels 11; Gaps

QY 1 MSNRDLGKVAIIITGTLGIGLAIAATKFFVEEGAKVNITDRHSDVGEKKAASVGTDPQIOFF 60
DB 1 MIMNLTKTVLITGASGIGYAQAQFLGQGANVVVADIDEAQCEAMVYKKN--DRLHFV 59
QY 61 QHDSDEGWTFLDPATEKAFQPSVTLVNNAGIAVKNVSVEETTAERKLLAVNLGDVGF 120
DB 60 QTDITDEACAOBAVESAVHTFGGLDLVLIINNAIEIAPIHMEIUSDWKNKVLQVNLTMFL 119
QY 121 GTRLGIORMKNKGLGASIIIMSSIEGFVGDPSLGAYNASKGAVRTMKSAAIDCALNDYD 180
DB 120 MSKHALKMLAAGK--NIINTCSVGLVAVFPDIPAYNASKGVQLTKMSMAVDFA--KHQ 176
QY 181 VRVNTVHPGVIKTPL-----VDDLPGA--EAMSQRT--TPMGHIGEPNDIAIYCVILAS 233
DB 177 IRVNCVCPGIIPTLNEKSFLENNEGTLEIKKEKAKVNPILLRLGKPEIANVMVFLASD 236
QY 234 ESKFATGSEFVVDGGYTAQ 252
DB 237 LSSYMTGSAITADGGYTAQ 255

RESULT 5
Y019_THEME
ID Y019_THEME STANDARD; PRT; 256 AA.
AC Q56318;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative oxidoreductase TM0019. (EC 1.-.-.-).
GN TM0019.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=96125254; PubMed=8550425;
RA Kletzin A., Adams M.;
RT "Molecular and phylogenetic characterization of pyruvate and 2-
RT ketoisovalerate ferredoxin oxidoreductases from Pyrococcus furiosus
RT and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.";
RN J. Bacteriol. 178:248-257(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RN Nature 398:323-329(1999).
RN CC
RN CC -! SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
RN CC (SDR) FAMILY.
RN CC
RN CC -----
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DR	PROSITE; PS00061; ADH_SHORT; 1.
KW	Oxidoreductase; NAD; Steroid metabolism; 3D-structure.
NP_BIND	10 34 NAD (BY SIMILARITY).
FT	ACT_SITE 152 152
SQ	SEQUENCE 255 AA; 26484 MW; 9CB93CB66AA628D5 CRC64;
Query Match	31.6%; Score 407.5; DB 1; Length 255;
Best Local Similarity	39.0%; Pred. No. 2.8e-26;
Matches 97; Conservative 42; Mismatches 103; Indels 7; Gaps 5;	
QY	3 NRLDGKVAIIIGTGLIGLAIATKFEVEGAQVMTDRHSVDGEKAASKSVGTDPDIQIOPFH 62 : : : : :
DB	2 NDLSGGTVITIGTGARGLGAEAAQAAGAVVADVLDVLDEGAATAARELG--DAARYOHL 59 : : : : :
QY	63 DSDEIDGWTKLFDATEKAFGPSVTLVNNAGIAVNKSVEETTTAERWKLLAVNLGDGVFEGT 122 : : : : :
DB	60 DVTIEDQRVVAYAREEFGSDVCLVNNAGISTGMLETESVERFKVVDINLTGVFIGM 119 : : : : :
QY	123 RLGIORMKNGKLGAASINNSSIIEGFCDPSLGAYNASKGAVRIMSKSAALDCALKDYDVR 182 : : : : :
DB	120 KTVIPAMKDAG-GGSIVNTSSRAAGLMGLALTSSYGASKWGVRGLSKLAAVE--LGTDRIR 176 : : : : :
QY	183 VNTVHPGYIKTPLVDPLPGAAEAAMSORTITPMGHIG-EPNDTAYICVYLASNESKFATQS 241 : : : : :
DB	177 VNSVHFEGMTPTMAEE-TGIROGEGNYPNTPMGRVGNEFEIAGAAYVKLLSSTSYVTGA 235 : : : : :
QY	242 EFVVDGGYT 250
DB	236 ELAVDGGWT 244
RESULT 4	
ID YWFD_BACSU STANDARD; PRT; 255 AA.	
AC P39640;	
DT 01-FEB-1995 (Rel. 31, Created)	
DT 01-FEB-1995 (Rel. 31, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Hypothetical oxidoreductase ywfd (EC 1.-.-.-).	
DN YWFD OR IPA-82D.	
GN Bacillus subtilis.	
OS Bacteria; Firmicutes; Bacillus/Clostridium group;	
OC Bacillus/Staphylococcus group; Bacillus.	
OX NCBI_TaxId=1423;	
[1]	
RN SEQUENCE FROM N.A.	
RP STRAIN=168;	
RC MEDLINE=95020537; PubMed-7934828;	
RR Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,	
RA Hulio M.F., Inesescu M., Lubochinsky E., Marcelino L., Moszer I.,	
RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,	
RA Rapoport G., Danchin A.;	
RT "Bacillus subtilis genome project: cloning and sequencing of the 97	
RT kb region from 325 degrees to 333 degrees.";	
RL Mol. Microbiol. 10:371-384(1993).	
CC -1. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDOGENASES/REDUCTASES	
CC (SDR) FAMILY.	
CC -----	
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CC or send an email to licensese@isb-sib.ch).	
CC -----	
EMBL; X73124; CAAS1638.1; --	
DR EMBL; Z99123; CABIS1599.1; --	
DR PIR; S39737; S39737.	
DR HSP; P50162; 1AEL	
DR SubtilList; BG10628; ywfd.	
DR InterPro; IP002198; ADH_short.	
DR Pfam; PF00106; adh_short; 1.	


```

RN  SEQUENCE FROM N.A.
RP  STRAIN-1AM 1030;
RC  Mitamura T., Ehora R.V., Nakai T., Makino Y., Negoro S., Urabe I.,
RA  Okada H.;
RT  "Structure of isozyme genes of glucose dehydrogenase from Bacillus
RJ  megaterium IAM1030."
RL  J. Ferment. Bioeng. 70:363-369(1990).
CC  -!- FUNCTION: MAY PLAY SOME ROLE IN SPORE GERMINATION.
CC  -!- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) = D-glucono-1,5-
CC  lactone + NAD(P)H.
CC  -!- SUBUNIT: HOMOTETRAMER.
CC  -!- DEVELOPMENTAL STAGE: EXPRESSED DURING SPORULATION.
CC  -!- MISCELLANEOUS: PREFERS NADP TO NAD.
CC  -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC  (SDR) FAMILY.
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D90043; BAAL4099.1;
DR  PIR; JS0385; JS0385.
DR  HSSP; P50163; 2AE1.
DR  InterPro; IPR002198; ADH_short.
DR  Pfam; PF00106; adh_short; 1.
DR  PRINTS; PR00080; SDRFAMILY.
DR  PROSITE; PS00061; ADH_SHORT; 1.
KW  Oxidoreductase; NADP; Multigene family; Sporulation; Germination.
FT  NP_BIND 11 35 NADP (BY SIMILARITY).
FT  ACT_SITE 158 158 BY SIMILARITY.
FT  SEQUENCE 261 AA; 28117 MW; B92B7288A160335 CRC64;

Query Match 28.8%; Score 371.5; DB 1; Length 261;
Best Local Similarity 34.2%; Pred. No. 2.5e-23;
Matches 88; Conservative 51; Mismatches 105; Indels 13; Gaps 5;

QY 1 MSNRDGGKVAITGGTGLGIGLAIAATKVFEEGAKVMTDRHSDVGEKA-----AKSVGTP 54
DB 1 MYKDLGKVVVITGGTGLGKSMATFPATEKAKVVVNYRSKE--EANSVLVEIKKVG-- 56

QY 55 DQIQFFQHDSDDEGWTGLFDATKAFGPVSTLVNAGIAVNKSVETTTAEWRKLLAVN 114
DB 57 GEALAVKGDVTVESDVINLVQSSIKFEGKLDVMINNAGHENPVSSHMSLSDNKVIDTN 116

QY 115 LDGVFFGTRGLGIORMKNKGLGASIIINMSSIEGFVGDPSLGAYNASKGAVRIMSKSAALDC 174
DB 117 LTGAFLGSRKAIKVFVENDIKGTVINMSSVHEKIPWPLFVHYAASKGKMLMTETLLEY 176

QY 175 ALKDYDVRVNTVHPGYIKTPL-VDDLPGAEEAMSORTKTPMGHIGEPNDIAICVILASN 233
DB 177 APK--GIRVNNIGPGAINTPINAEKPADPQADVESMIPMGYIGEPEEIAAVALASS 234

QY 234 ESKFATGSEFVVDGGYT 250
DB 235 EASYVTGITLFDAGGMT 251

RESULT 8
DHG_BACME STANDARD; PRT; 261 AA.
AC P40288.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glucose 1-dehydrogenase (EC 1.1.1.47).
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;

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RN  SEQUENCE FROM N.A., SEQUENCE OF 1-29, AND MUTAGENESIS.
RP  STRAIN-IMG3;
RC  MEDLINE-89197943; PubMed-2495285;
RA  Makino Y., Negoro S., Urabe I., Okada H.;
RT  "Stability-increasing mutants of glucose dehydrogenase from Bacillus
RJ  megaterium IMG3."
RL  J. Biol. Chem. 264:6381-6385(1989).
CC  [2]
CC  REVISIONS.
CC  Urabe I.;
CC  Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
CC  -!- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) = D-glucono-1,5-
CC  lactone + NAD(P)H.
CC  -!- SUBUNIT: HOMOTETRAMER.
CC  -!- DEVELOPMENTAL STAGE: EXPRESSED DURING SPORULATION.
CC  -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC  (SDR) FAMILY.
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; J04805; AAA22475.1;
DR  PIR; A33528; A33528.
DR  HSSP; P50163; 2AE1.
DR  InterPro; IPR002198; ADH_short.
DR  Pfam; PF00106; adh_short; 1.
DR  PRINTS; PR00080; SDRFAMILY.
DR  PROSITE; PS00061; ADH_SHORT; 1.
KW  Oxidoreductase; NADP; Multigene family; Sporulation.
FT  NP_BIND 11 35 NADP (BY SIMILARITY).
FT  ACT_SITE 158 158 BY SIMILARITY.
FT  MUTAGEN 96 96 E->A,G,K; HEAT STABLE.
FT  MUTAGEN 108 108 D->N; HEAT STABLE.
FT  MUTAGEN 112 112 V->A; HEAT STABLE.
FT  MUTAGEN 133 133 E->K; HEAT STABLE.
FT  MUTAGEN 183 183 V->I; HEAT STABLE.
FT  MUTAGEN 194 194 P->Q; HEAT STABLE.
FT  MUTAGEN 210 210 E->K; HEAT STABLE.
FT  MUTAGEN 217 217 Y->H; HEAT STABLE.
FT  MUTAGEN 252 252 Q->L; HEAT STABLE.
FT  MUTAGEN 253 253 Y->C; HEAT STABLE.
FT  MUTAGEN 258 258 A->G; HEAT STABLE.
SQ  SEQUENCE 261 AA; 28085 MW; C23AC98D304EEB2F CRC64;

Query Match 28.7%; Score 370.5; DB 1; Length 261;
Best Local Similarity 33.6%; Pred. No. 3e-23;
Matches 86; Conservative 51; Mismatches 108; Indels 11; Gaps 4;

QY 1 MSNRDGGKVAITGGTGLGIGLAIAATKVFEEGAKVMT-----DRHSDVGEKAASVGTGP 55
DB 1 MYKDLGKVVVITGGTGLGKSMATFPATEKAKVVVNYRSKEDEANSVLVEIKKVGGEAI 60

QY 56 QIQFFQHDSDDEGWTGLFDATKAFGPVSTLVNAGIAVNKSVETTTAEWRKLLAVN 115
DB 61 AV---KGDVTVESDVINLVQSAIKFEGKLDVMINNAGLENPVSSHMSLSDNKVIDTN 117

QY 116 DGVFEFTRGLGIORMKNKGLGASIIINMSSIEGFVGDPSLGAYNASKGAVRIMSKSAALDC 175
DB 118 TGAFLGSRKAIKVFVENDIKGTVINMSSVHEKIPWPLFVHYAASKGKMLMTETLLEYA 177

QY 176 LKDYDVRVNTVHPGYIKTPL-VDDLPGAEEAMSORTKTPMGHIGEPNDIAICVILASN 234
DB 178 PK--GIRVNNIGPGAINTPINAEKPADPQADVESMIPMGYIGEPEEIAAVALASS 235

QY 235 SKFATGSEFVVDGGYT 250
DB 236 ASYVTGITLFDAGGMT 251

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FT ACT_SITE      154          BY SIMILARITY.
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SQ SEQUENCE    246 AA;   26401 MW;   8C08904D28099142 CRC64;
```

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Query Match           28.3%; Score 365.5; DB 1; Length 246;  
Best Local Similarity 35.1%; Pred No. 7.1e-23;  
Matches 87; Conservative
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```
OY 4 RLDGKVAIIITGGTIGLGIAIATKFVEBGAKYMITDRHSVDGEKAASKV-GTPDOIQFFQH 62  
Db |||:||| |||| | : ||| | : | : | : | : | :  
2 RLEGVCLITGAASGICKATTLLFAQEAGTVIADISKENLDSLVKEAEGLPGRKDVPVL 61
```

```
OY 63 DSDDEDGWTKLFDATEAKAFPGVSTLYNNAGIANVKSVYEETTAERKLAVNLDGVFPFGT 122  
Db : : || : : : : ||||| : | : | : | : | : ||| |||  
62 NVTDROOIKEVKVWKVQRYGRIDVLVNNGITRDALLVRMKEEDWADVINVNLKGVENVT 121
```

```
OY 123 RLGIORMKNRGLGASIINMSIEGFVGDPISLGAYNASKGAVRIKSAALDCALKDYDV 182  
Db : : | : | : ||| : | : | ||| | : | : | : | : | : |||  
122 QMWVPYNIKORNG-SIVNVSSVVIYGNGPQTAAASKAGVIGMTKTWAKELAGR--NIR 178
```

```
OY 183 VNTVFHGYIKTPLDDPLP--GAEAMSORRTKTPMGHGEPNDIAYICVYLASNESKEFATG 240  
Db || ||| |: | : || : | : | : | : | : | : | : | : | : ||  
179 VNAPVAFGTETPTWEKLPKARETALS---RIPLRGFKPEEVAQVILFLASDESSVYTG 235
```

```
OY 241 SEFWDDG 248  
      : |||
```

```
DB 236 QTVIDGG 243
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```
RESULT 11
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DHGA_BACME STANDARD; PRT; 261 AA.  
ID AC DHGA_BACHE FLO528;  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OX Bacillus/Staphylococcus group; Bacillus.  
NCBI_TaxId=1404;  
RN [1]  
RC STRAIN=M1286;  
RP MEDLINE=68371315; PubMed=3134196;  
RA Heilmann H.J., Maegerl H.J., Gassen H.G.;  
RT Identification and isolation of glucose dehydrogenase genes of  
RL Bacillus megaterium M1286 and their expression in Escherichia coli.*;  
CC Eur. J. Biochem. 174:485-490(1988).  
CC -|- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) = D-glucono-1,5-lactone + NAD(P)H.  
CC -|- SUBUNIT: HOMOTETRAMER.  
CC -|- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
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EMBL: X12370; CAAB30931.1; --  
PIR: S00812; S00812.  
WSP: PS0162; IAEI.  
InterPro: IP0002198; ADH_short.  
PFam: PF00106; adh_short; 1.  
PRINTS: PR00080; SDREAMELY.  
PROSITE: PS00061; ADH_SHORT; 1.  
Okidoreductase; NADP; Multigene family.  
NP_BIND 11 35             NADP (BY SIMILARITY).  
FT ACT_SITE 158 158      BY SIMILARITY.
```

RA Froschle M., Ulmer W., Jany K.-D.;
 RT "Tyrosine modification of glucose dehydrogenase from *Bacillus*
 RT megaterium. Effect of tetranitromethane on the enzyme in the
 RT tetrameric and monomeric state.";
 RL Eur. J. Biochem. 142:533-540(1984).
 CC -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-
 CC lactone + NAD(P)H.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING SPORULATION.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR PIR: S02299; S02299.
 DR PIR: S01227; S01227.
 DR PIR: A20238; A20238.
 DR PIR: B20238; B20238.
 DR PIR: C20238; C20238.
 DR PIR: D20238; D20238.
 DR PIR: A23260; A23260.
 DR PIR: A23260; A23260.
 DR HSP: P50163; 2AE1.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; NADP; Multigene family; Sporulation.
 FT NP_BIND 11 35 NADP (BY SIMILARITY).
 FT ACT_SITE 160 160 BY SIMILARITY.
 SQ SEQUENCE 262 AA; 28347 MW; C9281328D634E789 CRC64;

Query Match 27.9%; Score 360; DB 1; Length 262;
 Best Local Similarity 34.2%; Pred. No. 2.2e-22;
 Matches 88; Conservative 51; Mismatches 106; Indels 12; Gaps 6;

QY 1 MSNRDGVKVAITGGTIGLAIATKVEEGAKVMIT-----DRHSDVGEKAASVGPDP 55
 Db 1 MYKDLEKVVVITGSSGTGSKMAIRFATEKAKVVVYRSKEDEANSVLEEIKVGG-G 58
 QY 56 QIQFFHSDSDGWTGLFDATEKAFGVPSTLVNAGIANKSVSEETTTAEWRKLLAVNL 115
 Db 59 EATAVKGDTVESDVINLVQSAKEFGKLDVMINNAGMENPVSSHMSLSDNKVIDTNL 118
 QY 116 DGVFFGTGLQRMKNKGLGASIIINMSI-EGFVGDPSLGAYNASKGAVRIMSKSAALDC 174
 Db 119 TGAFLGSRKAKYFVENDIKGTVINMSVHEWIPWPLFVHYAASKGKMLTETLLEY 178
 QY 175 ALKDYDVRVNTVHPGYIKTKPL-VDDLPGAEAMSQRTKTPMGHIGEPNDIAYICVILASN 233
 Db 179 APR--GIRVNIIGPGAINTPINAEKPADPEORADVESMIPMGYIGEPEEIAAV-AWLASS 235
 QY 234 ESKFATGSEFVDDGGYT 250
 Db 236 EASYVTGTLFADGGMT 252

RESULT 13
 DHG_BACSU STANDARD; PRT; 261 AA.
 ID F12310; P94430;
 AC 01-OCT-1989 (Rel. 12, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glucose 1-dehydrogenase (EC 1.1.1.47).
 GN GDH.
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; *Bacillus*/Clostridium group;
 OC *Bacillus*/Staphylococcus group; *Bacillus*.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86168021; PubMed=3082854;
 RA Lampel K.A., Uratani B., Chaudhry G.R., Ramaley R.F., Rudikoff S.;
 RT "Characterization of the developmentally regulated *Bacillus subtilis*
 RT glucose dehydrogenase gene.";
 RL J. Bacteriol. 166:238-243(1986).

(2)
 RN SEQUENCE FROM N.A.
 RP STRAIN=168;
 RC MEDLINE=97124189; PubMed=8969502;
 RA Yamane K., Kumano M., Kurita K.;
 RT "The 25 degrees-36 degrees region of the *Bacillus subtilis* chromosome:
 RT determination of the sequence of a 146 kb segment and identification
 RT of 113 genes.";
 RL Microbiology 142:3047-3056(1996).
 CC -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) -> D-glucono-1,5-
 CC lactone + NAD(P)H.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- INDUCTION: IT IS INDUCED AT STAGE III OF THE SPORULATION.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC -----
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 CC -----
 DR EMBL: M12276; AAA22463.1; -
 DR EMBL: D50453; BAA09024.1; -
 DR EMBL: Z99106; CAB12201.1; -
 DR PIR: S36090; S36090.
 DR HSP: P50162; 1AE1.
 DR Subtilist; BG10545; gdh.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam: PF00106; adh_short; 1.
 DR PRINTS: PR00080; SDRFAMILY.
 DR PROSITE: PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; NADP; Sporulation; Complete proteome.
 FT NP_BIND 11 35 NADP (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT CONFLICT 148 150 EVI -> AF (IN REF. 1).
 SQ SEQUENCE 261 AA; 28090 MW; 5894C17DB8F14965 CRC64;

Query Match 27.8%; Score 358.5; DB 1; Length 261;
 Best Local Similarity 33.9%; Pred. No. 2.8e-22;
 Matches 87; Conservative 45; Mismatches 104; Indels 21; Gaps 5;

QY 5 LDGKVAITGGTIGLAIATKVEEGAKVMIT-----DRHSDVGEKAASVGPDPQIQF 59
 Db 5 LKGVVAITGAASGLGKMAIRFGEQAKVVVINYSKQDPNEKVEIKAGG---EAVV 61
 QY 60 FQHDSDGWTGLFDATEKAFGVPSTLVNAGIANKSVSEETTTAEWRKLLAVNLGVF 119
 Db 62 VQGDVTKEDVKNIQVTAKEFGTGLDINNAGLENVPVSHENPLKDKDKVIGTINLGAF 121
 QY 120 FGRGLGQRMKNKGLGASIIINMSIEFGVGDPSLGAYNASKGAVRIMSKSAALCALDY 179
 Db 122 LGSREAIKYEVDIKGNVINMSVHEVWPWPLFVHYAASKGKIKMTETLLEYAPK-- 179
 QY 180 DVRVNTVHPGYIKTKPLVDLPGAEAMSQRTK-----PMGHIGEPNDIAYICVILASN 233
 Db 180 GIRVNIIGPGAINTPI-----NAEKFPADPKOKADVESMIPMGYIGEPEEIAAVAWLASK 234
 QY 234 ESKFATGSEFVDDGGYT 250
 Db 235 EASYVTGTLFADGGMT 251

RESULT 14
 DHG4_BACME STANDARD; PRT; 261 AA.
 ID AC B39485;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glucose 1-dehydrogenase IV (EC 1.1.1.47) (GLCDH-IV).

GN DHIV.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-1AM 1030;
RA Nagao T., Mitamura T., Wang X.H., Negoro S., Yomo T., Urabe I.,
RA Okada H.;
RT Cloning, nucleotide sequences, and enzymatic properties of glucose
RT dehydrogenase isozymes from Bacillus megaterium IAM1030.*;
RL J. Bacteriol. 174:5013-5020(1992).
CC -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) = D-glucono-1,5-
CC lactone + NAD(P)H.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- MISCELLANEOUS: PREFERENCES NAD TO NADP; 2M NaCl ENHANCES ITS PH AND
CC THERMOSTABILITY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; D10266; BAA01476.1;
DR HSP; P50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Multigene family.
FT NP_BIND 11 35 NAD (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
SQ SEQUENCE 261 AA; 28157 MW; 6FBE9397BCF417C CRC64;

Query Match 27.7%; Score 357.5; DB 1; Length 261;
Best Local Similarity 32.1%; Pred. No. 3.4e-22;
Matches 85; Conservative 51; Mismatches 100; Indels 29; Gaps 6;

QY 1 MSNRLDGKVAITGTGTLGIGLAIAATKFEVEGAKVMT-----DRHSDVGERAAKSV 51
DB 1 MYTDLKDKVVVITGSGTGLGRAMAVRFGQEKVINYNNNEEALDAKVEEAGGQAI 60
QY 52 GTPDQIQFFQHDSSDEGWTKLFDATKAFGPVSTLVNNAIYAVKNSVEETTTAEWRKLL 111
DB 61 -----IVQGDVTKEDVNVLVQTAIREFGTLDVNNAGVENPVPSHELSDNNKVI 113
QY 112 AVNLDGVFEGTRIGIQRKMKNGKLGASINSSIEGFGVDPSPGAYNASKGAVRIMSKSA 171
DB 114 DPNLGAFLGSREAIKYFVENDIKGNVINSSVHEMIPWPLFVHYAASKGGMKLTETLA 173
QY 172 LDCALKDYRVNTVHPGYIKTPL-----VDLPGAE-EAMSQRTKTPMGHIGEPNDIAY 225
DB 174 LEYAPK--GIRVNNIGPGAMTNPINAEKFPADVPQRADVESM-----IPMGYIGKPEEVA 226
QY 226 ICYLLASNEKFCATGSEFYVDGGYT 250
DB 227 VAAFLASSQASVVTGTLTADGGMT 251

RESULT 15
DHG2_BACME STANDARD; PRT; 261 AA.
AC DHG2_BACME
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Glucose 1-dehydrogenase II (EC 1.1.1.47) (GLCDH-II).
GN GDHII.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-1AM 1030;
RA Mitamura T., Ebara R.V., Nakai T., Makino Y., Negoro S., Urabe I.,
RA Okada H.;
RT *Structure of isozyme genes of glucose dehydrogenase from Bacillus
RT megaterium IAM1030.*;
RL J. Ferment. Bioeng. 70:363-369(1990).
CC -1- CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) = D-glucono-1,5-
CC lactone + NAD(P)H.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- MISCELLANEOUS: PREFERENCES NADP TO NAD.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; D90044; BAA14100.1;
DR HSP; P50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Multigene family.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
SQ SEQUENCE 261 AA; 28251 MW; CEF9AA1425D2999C CRC64;

Query Match 27.6%; Score 355.5; DB 1; Length 261;
Best Local Similarity 31.4%; Pred. No. 5e-22;
Matches 80; Conservative 55; Mismatches 111; Indels 9; Gaps 4;

QY 1 MSNRLDGKVAITGTGTLGIGLAIAATKFEVEGAKVMTDRHSDVG-----EKAASVCTPDQ 56
DB 1 MYTDLKDKVVVITGSGTGLGRAMAVRFGQEKVINYNNNEEALDAKVEEAGGQAI 58
QY 57 IQFFQHDSSDEGWTKLFDATKAFGPVSTLVNNAIYAVKNSVEETTTAEWRKLLAVNLD 116
DB 59 ALIVRGDVTKEEDVNVLVQTAIREFGTLDVNNAGVENPVPSHELSDNNKVI 118
QY 117 GVFFGTRIGIQRKMKNGKLGASINSSIEGFGVDPSPGAYNASKGAVRIMSKSAALDCA 176
DB 119 GAFLGSREAIKYFVENDIKGNVINSSVHEMIPWPLFVHYAASKGGMKLTETLALEYAP 178
QY 177 KYDVRVNTVHPGYIKTPL-----VDLPGAE-EAMSQRTKTPMGHIGEPNDIAYICVYLAS 235
DB 179 K--GIRVNNIGPGAMTNPINAEKFPADVPQRADVESM-----IPMGYIGKPEEVAFLASSQA 236
QY 236 KFATGSEFYVDGGYT 250
DB 237 SVVTGTLTADGGMT 251

Search completed: October 30, 2002, 15:45:26
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 30, 2002, 15:45:05 ; Search time 27 Seconds
(without alignments)
1614.619 Million cell updates/sec

Title: US-09-910-033a-2
Perfect score: 1290
Sequence: 1 MSNLDGKVAITGTLGIG.....NESKATGSEFVDGGVTAQ 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19:**
- 1: sp_archaea:**
 - 2: sp_bacteria:**
 - 3: sp_fungi:**
 - 4: sp_human:**
 - 5: sp_invertebrate:**
 - 6: sp_mammal:**
 - 7: sp_mhc:**
 - 8: sp_organelle:**
 - 9: sp_phase:**
 - 10: sp_plant:**
 - 11: sp_rodent:**
 - 12: sp_virus:**
 - 13: sp_vertebrate:**
 - 14: sp_unclassified:**
 - 15: sp_rvirus:**
 - 16: sp_bacteriap:**
 - 17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	470	36.4	261	16	Q9AB11	Q9ab11 caulobacter
2	452.5	35.1	250	2	Q937L4	Q937L4 comamonas t
3	438	34.0	254	2	Q9K4G9	Q9K4G9 streptomyce
4	411	31.9	251	2	Q9RNK5	Q9rnk5 zymomonas m
5	411	31.9	254	2	Q52587	Q52587 comamonas t
6	395.5	30.7	256	2	Q93QG5	Q93qg5 brevibacter
7	391	30.3	249	2	Q56841	Q56841 xanthobacte
8	386.5	30.0	247	2	Q93RM0	Q93rm0 acinetobact
9	386.5	30.0	251	2	Q9F7E0	Q9f7e0 acinetobact
10	378.5	29.3	258	2	Q9JN17	Q9jnl7 agrobacteri
11	376.5	29.2	255	16	Q98EN0	Q98en0 rhizobium l
12	374.5	29.0	248	16	Q31680	Q31680 bacillus su
13	374.5	29.0	250	16	Q98C53	Q98c53 rhizobium l
14	373	28.9	249	2	Q9L8C5	Q9l8c5 geobacillus
15	372.5	28.9	253	16	Q930L7	Q930l7 rhizobium m
16	370	28.7	246	2	Q9EX74	Q9ex74 rhodococcus

17	369.5	28.6	251	16	Q92PX8	Q92px8 rhizobium m
18	368	28.5	253	16	Q9CH41	Q9ch41 lactococcus
19	367	28.4	258	16	Q33339	Q33339 mycobacteri
20	366	28.4	272	16	Q99RG1	Q99rg1 staphylococ
21	364.5	28.3	255	16	P95286	P95286 mycobacteri
22	364	28.2	264	2	Q9AK65	Q9ak65 streptomyce
23	360	27.9	251	2	Q9FDK2	Q9fdk2 zymomonas m
24	359	27.8	256	16	Q982N5	Q982n5 rhizobium l
25	358	27.8	270	6	Q9WVP6	Q9wvp6 bos taurus
26	357.5	27.7	258	16	Q930L5	Q930l5 rhizobium m
27	357.5	27.7	261	2	Q9F5L5	Q9f5l5 bacillus su
28	357	27.7	296	16	Q9ABX6	Q9abx6 caulobacter
29	356.5	27.6	256	16	Q92MR3	Q92mr3 rhizobium m
30	351	27.2	286	16	Q911X3	Q911x3 pseudomonas
31	350	27.1	257	16	Q9WYD3	Q9wyd3 thermotoga
32	348.5	27.0	255	16	Q92RW7	Q92rw7 rhizobium m
33	347.5	26.9	268	17	Q9HLN6	Q9hln6 thermoplasm
34	347	26.9	243	16	Q9KCO9	Q9kcg9 bacillus ha
35	346.5	26.9	254	2	Q9RH24	Q9rh24 zymomonas m
36	346.5	26.9	255	16	Q9WYS2	Q9wys2 thermotoga
37	346.5	26.9	268	16	Q986J1	Q986j1 rhizobium l
38	346	26.8	248	2	Q923Y5	Q923y5 pseudomonas
39	345.5	26.8	261	2	Q9F2A6	Q9f2a6 bacillus l
40	345	26.7	248	16	Q987H1	Q987h1 rhizobium l
41	344.5	26.7	261	17	Q97CM7	Q97cm7 thermoplasm
42	344	26.7	303	10	Q9SCU0	Q9scu0 arabidopsis
43	343.5	26.6	250	2	Q56840	Q56840 xanthobacte
44	343.5	26.6	299	17	Q97UR6	Q97uk6 sulfolobus
45	343	26.6	255	17	Q9HK51	Q9hk51 thermoplasm

ALIGNMENTS

RESULT 1

Q9AB11	PRELIMINARY;	PRT;	261 AA.
ID Q9AB11			
AC Q9AB11			
DT 01-JUN-2001 (TREMBLrel. 17, Created)			
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL DEHYDROGENASE.			
GN CC0246.			
OS Caulobacter crescentus.			
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;			
OC Caulobacter.			
OX NCBI_TaxID=69394;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=ATCC 19089 / CB15;			
RX MEDLINE=21173698; Pubmed=11259647;			
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,			
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,			
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,			
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,			
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,			
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,			
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;			
RT "Complete genome sequence of Caulobacter crescentus.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).			
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES			
CC (SDR) FAMILY.			
DR EMBL; AE005698; AAK22233.1; -			
DR HSSP; P19992; 1HDC.			
DR TIGR; CC0246; -			
DR InterPro; IPR002198; ADH_short.			
DR Pfam; PF00106; adh_short; 1.			
DR PRINTS; PR00080; SDRFAMILY.			
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.			
KW Complete proteome; Oxidoreductase.			
SQ SEQUENCE 261 AA; 27011 MW; CE011D872D4EBA6D CRC64;			

Query Match 36.4%; Score 470; DB 16; Length 261;

DE	BETA-HYDROXYSTEROID DEHYDROGENASE.	
OS	Zymomonas mobilis.	
OC	Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;	
OC	Zymomonas.	
OX	NCBI_TaxID=542;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ZM4;	
RA	Lee H.J., Kang H.S.;	
RT	*Sequence analysis of 42f4 fosmid clone of Zymomonas mobilis ZM4.*;	
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.	
DR	EMBL; AF180145; AAD56922.1; -.	
DR	HSSP; PI19992; LHDC.	
DR	InterPro; IPR002198; ADH_short.	
DR	Pfam; PF00106; adh_short; 1.	
DR	PRINTS; PR00080; SDRFAMILY.	
KW	Oxidoreductase.	
QY	SEQUENCE 251 AA; 26621 MW; 62DD151CAFA7CF6B CRC64;	
QY	Query Match 31.9%; Score 411; DB 2; Length 251;	
DB	Best Local Similarity 40.6%; Pred. No. 2.le-23;	
DB	Matches 101; Conservative 33; Mismatches 95; Indels 20; Gaps 5;	
QY	14 GGTIGIGIATKTFVEGAKVWIDRISDVGEKAASVGTGPDQIQFFQHDSSDEDGWTKL 73	
DB	: : : : : : : : : :	
QY	5 GCARGIGRAIAAAPHQHEGAKVIVTDIDVTGKTKAAEITGG---QFOKLDVREEKQWNL 60	
DB	: : : : : : : : : : : : : : :	
QY	74 FDATEKAFGVPVSTLVNAGI-----AVNKSVEETTTAEWRKLLAVNLDGVFFGTRLGIQ 127	
DB	: : : : : : : : : : : :	
QY	61 AEIVP-----VVDVVNNGITGFENGVAHDPEHATLEDHRAVHRVNLDCGFLGCRYAIA 116	
DB	: : : : : : : : : : : :	
QY	128 RMNKGILGASIIINSSIEGEGVDPISLAYNASKGAVRIMSKSAALDCALKDYDVRVNTVH 187	
DB	: : : : : : : : : : : :	
QY	117 AMNKGKG- SIINISSRSLGVLPIAAYASSKAAIRNHSKVALYCAQOGWKTRCHNAIN 175	
DB	: : : : : : : : : : : : : : :	
QY	188 PGYIKTPLVLDLPGAEAMGORTK-----TPMGHIGPNDIAYTCVILASNESKFATGSE 242	
DB	: : : : : : : : : : : : : : :	
QY	176 PAALTSIWEPMLGDDGDRKRMQALVADTPLKRFGLPEEVAAVAVMLASDEATYMTGAE 235	
DB	:	
QY	243 FVVDGGYTA 251	
DB	:	
QY	236 FNIDGGLLA 244	
DB	:	
RESULT 5		
Q52587	PRELIMINARY; PRT; 254 AA.	
ID	Q52587	
AC	Q52587;	
DT	01-NOV-1996 (Tremblrel. 01, Created)	
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)	
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)	
DE	BETA-HYDROXYSTEROID DEHYDROGENASE.	
OS	Comamonas testasteroni (Pseudomonas testasteroni).	
OC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.	
OX	NCBI_TaxID=285;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ATCC 11996;	
RA	Cabrera J.E., Gentil-Raimondi S.;	
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.	
DR	EMBL; U41265; AAA25742.1; -.	
DR	HSSP; PI19992; LHDC.	
DR	InterPro; IPR002198; ADH_short.	
DR	Pfam; PF00106; adh_short; 1.	
DR	PRINTS; PR00080; SDRFAMILY.	
DR	PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.	
KW	Oxidoreductase.	
QY	SEQUENCE 254 AA; 26952 MW; FB6EC90B151975DB CRC64;	

Db 65 NKANTAEPEDKAAVEFAVSTGALHLAFNNAGILGEVN-STEELSIEGWRVIDVNLNA 123
Qy 118 VFGTRGLQRMKNKGLGASIIINSSIEGFGVDPSPSLGAYNASKGAVRIMSKSAALDCALK 177
Db 124 VFSYMHYEPAILAAG-GGAIVNTASIAGLIGIONISGVAAGKGVGTGLTKAAALEYA-- 180
Qy 178 DYDVRVNTVHPGYIKTPTLVDDLPGLGAEEAMSQRTKTPMGHIGEPNDIAYICVILASNEKF 237
Db 181 DKGIIRNSVHPGYIKTPTLVDDLPGLGAEEAMSKLH---PIGLGQPEEVAQVAFLLSDASF 236
Qy 238 ATGSEFVVDGYTAQ 252
Db 237 VTGSQVVDGYTSK 251

RESULT 10
Q9JN17
ID Q9JN17 PRELIMINARY; PRT; 258 AA.
AC Q9JN17
DT 01-OCT-2000 (TremBLrel. 15, Created)
DE 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE YHG.
GN YHG.
OS Agrobacterium tumefaciens.
OG Plasmid T1.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE OF 1-6 FROM N.A.
RX MEDLINE=96236046; PubMed=8655509;
RA Kim K.S., Farrand S.K.;
RT "Ti plasmid-encoded genes responsible for catabolism of the crown gall
RT opine mannopine by Agrobacterium tumefaciens are homologs of the T-
RT region genes responsible for synthesis of this opine by the plant
RT tumor.";
RT J. Bacteriol. 178:3275-3284(1996).
RN [2]
RP SEQUENCE OF 4-258 FROM N.A.
RX MEDLINE=99141607; PubMed=9987134;
RA Lyi S.M., Jafri S., Winans S.C.;
RT "Mannopinic acid and agropinic acid catabolism region of the octopine-
RT type Ti plasmid pTi15955.";
RL Mol. Microbiol. 31:339-347(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
RA Farrand S.K.;
RT "Octopine-type Ti plasmid sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY
DR EMBL; AF242881; AAF77146.1; --
DR HSPF; P50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Oxidoreductase; plasmid.
SQ SEQUENCE 258 AA; 27591 MW; B4E4D0364468C44C CRC64;

Query Match 29.3%; Score 378.5; DB 2; Length 258;
Best Local Similarity 37.6%; Pred. No. 6.1e-21;
Matches 97; Conservative 40; Mismatches 102; Indels 19; Gaps 6;
Qy 4 RLDGKVAITGTLGIGLAIAATKFEVGEAKVMTDRHSDVGEKAASVGTPTDQIOFFOHD 63
Db 11 RLDGKVAITGTLGIGLAIAATKFEVGEAKVMTDRHSDVGEKAASVGTPTDQIOFFOHD 69
Qy 64 SSEDGWTKLDATEKAGFPVSTLVNNAIAVKNKSVETTTAEWRKLLAVNLGDVFFGTR 123
Db 70 LKTRACALVKKRVADDRGLDILINNAIANGDTPLFTEQOVRDVIATNVTETVWCQS 129

Qy 124 LGIQRMKNKGLGASIIINSSIEGFGVDP--PSLGAYNASKGAVRIMSKSAALDCALKDYDV 181
Db 130 AAIPVMEGGGGA-IVNMGSMGIVSNIPQNVAYNSSKAAVHMTKSLASELALD--NI 186
Qy 182 RVNTHVHPGYIKTPTLVDDLPGLGAEEAMSQRTK-----TPMGHIGEPNDIAYICVILASNE 234
Db 187 RVNTHVHPGYIKTPTLVDDLPGLGAEEAMSKLH---PIGLGQPEEVAQVAFLLSDASF 240
Qy 235 SKFATGSEFVVDGYTAQ 252
Db 241 SSYVTGDLVVDGYTTR 258
RESULT 11
Q98EN0
ID Q98EN0 PRELIMINARY; PRT; 255 AA.
AC Q98EN0
DT 01-OCT-2001 (TremBLrel. 18, Created)
DE 01-OCT-2001 (TremBLrel. 18, Last sequence update)
DE 01-OCT-2001 (TremBLrel. 18, Last annotation update)
DE SHORT-CHAIN DEHYDROGENASE.
GN MLR4172.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003003; BAB50888.1; --
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Complete proteome.
SQ SEQUENCE 255 AA; 26441 MW; 7EAF89BB46810117 CRC64;

Query Match 29.2%; Score 376.5; DB 16; Length 255;
Best Local Similarity 38.3%; Pred. No. 8.4e-21;
Matches 101; Conservative 37; Mismatches 103; Indels 23; Gaps 7;
Qy 1 MSNRLDGRVAITGTLGIGLAIAATKFEVGEAKVMTDRHSDVGEKAASVGTPTDQI-QF 59
Db 1 MGERLAGRVAISGGATGCGGNASELFPAEGAKVAIIDENGAAATAAARARGEVAEH 60
Qy 60 FOHDSSDE-DGWTKLDATEKAGFPVSTLVNNAIAVKNKSVETTTAEWRKLLAVNLGDV 118
Db 61 FVADVSDEAQVAAVKGATEK-LGPVTVLFNAGTVIKPFLVETTTAEWRKLLAVNLGDV 119
Qy 119 FFGFELGTRMKNKGLGASIIINSSIEGFGVDPSPSLGAYNASKGAVRIMSKSAALDCALKD 178
Db 120 FLMTAVLPGVMIAG-GGSIVCTSSISAVAAPTPMEVLDTTKGACHMFARAIATVE--FRD 176
Qy 179 YDVRVNTVHPGYIKTPTLVDDLPGLGAEEAMSQRTKTPMGHIGEPNDIAYIC 227
Db 177 RNIRCNVCPGFIRTPHGLREVADLGKLGVDVSDAALAAQ-----GRIGEPVEVAKAA 230
Qy 238 VYLASNEKSFATGSEFVVDGYTA 251
Db 231 LYLASDESSFVNGAHLFVDNGFTA 254
RESULT 12
O31680
ID O31680 PRELIMINARY; PRT; 248 AA.

O31680;
 01-JAN-1998 (TREMBLrel. 05, Created)
 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE YKVO PROTEIN.
 GN YKVO.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
 Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 Parro V., Pohl T.M., Portetlelle D., Porwollik S., Prescott A.M.,
 Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 Sato T., Scanlon E., Schleich S., Schroeter R., Scoffone F.,
 Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis."
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 DR EMBL; Z99111; CAB13250.1; -;
 DR HSSP; P47227; 1BD8.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF0106; adh_short; 1.
 KW Complete proteome: Oxidoreductase.
 SQ SEQUENCE 248 AA; 26245 MW; EACA490C1239524D CRC64;
 Query Match 29.0%; Score 374.5; DB 16; Length 248;
 Best Local Similarity 37.5%; Pred. No. 1.2e-20;
 Matches 93; Conservative 40; Mismatches 106; Indels 9; Gaps 5;
 QY 4 RLDGKVAITGGTGLGIGLAIAATKFEVGGAKVMTDRHSDVGEKAASVGPDPQIOFFQHD 63
 DB 3 KFEGLIAVTGGTSGIGLATAQKFEVNEGAVVITGRQNELDKAVNIG--KNVTGVQGD 60
 QY 64 SDEDGWTGLFDATEKAFGPVSTLVNNAIVNKSVEETTTAEWRKLLAVNLGVPFGFR 123
 DB 61 ISKLEDLDLYDIKQEKGLDLIFANAGIGNFLPLGEITEEQVDRFTDINVKGTFTTQ 120
 QY 124 LGTQRMKNKGLGASIIINMSIEGFGVDPDPSLGAYNASKGAVRIMSKSAALDCAKLDYDVRV 183
 DB 121 KALPLFKD---GGSIILNSSVSNVGLPGFSTYAAKAAVRNFSRAWTLE--LKDKIRV 175
 QY 184 NTVHPGIYTKPLVDDLPG-----AEEAMSO-RFTKTPMGHIGEPNDIAYICVYLASNESKF 237
 DB 176 NTPSPGAIETPALETTLTGLTPEQAQVAQAFASQIPWGRGKPEETIAAAVTFLASDDSSY 235
 QY 238 ATGSEFVDDGG 248
 DB 236 VTGVDLAVDDGG 246
 RESULT 14
 QYLBGS
 ID QYLBGS PRELIMINARY; PRT; 249 AA.
 AC QYLBGS;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

Db 121 KALSFPDK--VGSIIVTGSTAGSIGNPAFSVYGASKAALRALVRNWILD--LKGTEIRV 176
 QY 184 NTVHPGIYTKPLVDDLPG--AEEAM-SORTKTPMGHIGEPNDIAYICVYLASNESKFATG 240
 Db 177 NVSPFGGILTPAYDELFGDALEEVLENSRNTVPAGKVGTPPEEVANAVSFLASDESSYLTG 236
 QY 241 SEFVDDGG 248
 Db 237 VELFVDDGG 244
 RESULT 13
 QYLBGS
 ID QYLBGS PRELIMINARY; PRT; 250 AA.
 AC QYLBGS;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE GLUCOSE DEHYDROGENASE.
 GN MLE5280.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti."
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003006; BAB51758.1; -;
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF0106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 KW Complete proteome.
 SQ SEQUENCE 250 AA; 26407 MW; 1736D8C3F6711274 CRC64;
 Query Match 29.0%; Score 374.5; DB 16; Length 250;
 Best Local Similarity 37.1%; Pred. No. 1.2e-20;
 Matches 93; Conservative 47; Mismatches 98; Indels 13; Gaps 5;
 QY 4 RLDGKVAITGGTGLGIGLAIAATKFEVGGAKVMTDRHSDVGEKAASVGPDPQIOFFQHD 63
 DB 3 KLECKIAVTGGSGIGLATAKRFVEGAHVITGRREKELKEAAFI--MRNVTTVGD 60
 QY 64 SDEDGWTGLFDATEKAFGPVSTLVNNAIVNKSVEETTTAEWRKLLAVNLGVPFGFR 123
 DB 61 VSLELDRLIAVVKKHGHIDVLFANAGAGTIAPLAAATEAHFDQTFDYNKGLFTTQ 120
 QY 124 LGTQRMKNKGLGASIIINMSIEGFGVDPDPSLGAYNASKGAVRIMSKSAALDCAKLDYDVRV 183
 Db 121 KALPLFKD---GGSIILNSSVSNVGLPGFSTYAAKAAVRNFSRAWTLE--LKDKIRV 175
 QY 184 NTVHPGIYTKPLVDDLPG-----AEEAMSO-RFTKTPMGHIGEPNDIAYICVYLASNESKF 237
 DB 176 NTPSPGAIETPALETTLTGLTPEQAQVAQAFASQIPWGRGKPEETIAAAVTFLASDDSSY 235
 QY 238 ATGSEFVDDGG 248
 DB 236 VTGVDLAVDDGG 246
 RESULT 14
 QYLBGS
 ID QYLBGS PRELIMINARY; PRT; 249 AA.
 AC QYLBGS;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

